



SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES

<130> D0072.NP

<140> US 10,029,345

<141> 2001-12-20

<150> US 60,256,868

<151> 2000-12-20

<150> US 60,280,186

<151> 2001-03-30

<150> US 60,387,735

<151> 2001-05-01

<150> US 60,195,848

<151> 2001-04-05

<150> US 60,300,465

<151> 2001-05-25

<160> 203

<170> PatentIn version 3.0

<210> 1

<211> 144

<212> DNA

<213> HOMO SAPIENS

<400> 1

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catgcagggc ttggtcgaac aggt 144

<210> 2

<211> 48

<212> PET

<213> HOMO SAPIENS

<400> 2

Leu Val Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser
1 5 10 15

Leu Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln
20 25 30

Glu Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly

35

40

45

<210> 3
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 <213> HOMO SAPIENS

<400> 3
 gatgtcttctt gggccctctt gtggaacaca gtt

33

<210> 4
 <211> 11
 <212> PRT
 <213> HOMO SAPIENS

<400> 4

Asp Val Phe Trp Ala Leu Leu Trp Asn Thr Val
 1 5 10

<210> 5
 <211> 746
 <212> DNA
 <213> HOMO SAPIENS

<400> 5
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 ctgggtgctt ccggggccggc tggcggggaact ggcgtgtgac cggctccccg ccactacca 120
 gttctgtttg gacctggggc tgcggcacct ggtgtccctg acggagcgcg ggcacctca 180
 cagcgacagc tgccccggcc tcacctgca ccgcctgcgc atccccgact tctgccccgc 240
 ggcccccgac cagatcgacc gcttcgtgca gatcgtggac gaggccaaacg cagggggaga 300
 ggctgtggga gtgcaactgtg ctctgggctt tggccgcact ggcaccatgc tggcctgtta 360
 cctggtgaag gagcggggct tggctgcagg agatgcaatt gctgaaatcc gacgactacg 420
 accgggcccc atcgagacct atgagcagga gaaagcagtc ttccagttct accagcgaac 480
 gaaataaggg gccttagtac ccttctacca ggccctcact ccccttcccc atgttgtcga 540
 tggggccaga gatgaaggga agtggactaa agtattaaac cctctagctc ccattggctg 600
 aagacactga agtagccac ccctgcaggc aggtcctgat tgaaggggag gcttgtactg 660
 ctttgttgaa taaatgagtt ttacgaacca gggaaaaaaaa aaaaaaaaaa aaagaaaaaa 720
 aaaaaaaaaa aaaaaaaaaa aaagaa 746

<210> 6
 <211> 248
 <212> PRT

<314> HOMO SAPIENS

<320>

<321> VARIANT

<322> (162)..(162)

<323> wherein 'Xaa' is any amino acid.

<330>

<331> VARIANT

<332> (200)..(200)

<333> wherein 'Xaa' is any amino acid.

<340>

<341> VARIANT

<342> (203)..(203)

<343> wherein 'Xaa' is any amino acid.

<350>

<351> VARIANT

<352> (214)..(214)

<353> wherein 'Xaa' is any amino acid.

<360>

<361> VARIANT

<362> (224)..(224)

<363> wherein 'Xaa' is any amino acid.

<400> 6

Trp Pro Gly Arg Arg Arg Gly Gln Val Gly Ala Met Gly Val Gln Pro
1 5 10 15

Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu Ala Gly Leu Ala Leu
20 25 30

Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu Asp Leu Gly Val Arg
35 40 45

His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro His Ser Asp Ser Cys
50 55 60

Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro Asp Phe Cys Pro Pro
65 70 75 80

Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile Val Asp Glu Ala Asn
85 90 95

Ala Arg Gly Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg
100 105 110

Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys Glu Arg Gly Leu Ala
115 120 125

Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Pro Ile
130 135 140

Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr
145 150 155 160

Lys Xaa Gly Ala Leu Val Pro Phe Tyr Gln Ala Leu Thr Pro Leu Pro
165 170 175

His Val Val Asp Gly Ala Arg Asp Glu Gly Lys Trp Thr Lys Val Leu
180 185 190

Asn Pro Leu Ala Pro Ile Gly Xaa Arg His Xaa Ser Ser Pro Pro Leu
195 200 205

Gln Ala Gly Pro Asp Xaa Arg Gly Gly Leu Tyr Cys Phe Val Glu Xaa
210 215 220

Met Ser Phe Thr Asn Gln Gly Lys Lys Lys Lys Lys Lys Arg Lys Lys
225 230 235 240

Lys Lys Lys Lys Lys Lys Lys Arg
245

<210> 7
<211> 511
<212> DNA
<213> HOMO SAPIENS

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attacacaca acccaaccaa tacctacttt aatagattct tacaggaact taagcaggat 120
ggagttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180
ggaagcatcc aggttcgga ctggcctttt gatgatggta cagcaccatc cagccagata 240
attgataact ggttaaaact tatgaaaaat aaatttcattg aagatcctgg ttgttgatt 300
gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgcc tagctttaat 360
tgaagggtgga atgaaatatg aaaatgtagt acagttcatc agataaaaagt gacatggaac 420
ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gcttgcacct 480
cagaaatccc agaaataact gtttccttca g 511

<210> 8
<211> 170
<212> PRT
<213> HOMO SAPIENS

<220>
<221> Variant

<222> (49)..(49)
 <223> wherein 'Xaa' is any amino acid.

<227>
 <228> Variant
 <229> (156)..(156)
 <230> wherein 'Xaa' is any amino acid.

<236>
 <237> Variant
 <238> (142)..(142)
 <239> wherein 'Xaa' is any amino acid.

<240>
 <241> Variant
 <242> (110)..(110)
 <243> wherein 'Xaa' is any amino acid.

<250>
 <251> Variant
 <252> (121)..(121)
 <253> wherein 'Xaa' is any amino acid.

<260>
 <261> Variant
 <262> (127)..(127)
 <263> wherein 'Xaa' is any amino acid.

<270>
 <271> Variant
 <272> (155)..(155)
 <273> wherein 'Xaa' is any amino acid.

<400> 8

Met	Ala	Arg	Met	Asn	Leu	Pro	Ala	Ser	Val	Asp	Ile	Ala	Tyr	Lys	Asn
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Val	Arg	Phe	Leu	Ile	Thr	His	Asn	Pro	Thr	Asn	Thr	Tyr	Phe	Asn	Arg
			20					25					30		

Phe	Leu	Gln	Glu	Leu	Lys	Gln	Asp	Gly	Val	Thr	Thr	Ile	Val	Arg	Val
		35					40					45			

Xaa	Lys	Ala	Thr	Tyr	Asn	Ile	Ala	Leu	Leu	Glu	Lys	Gly	Ser	Ile	Gln
	50					55				60					

Val	Pro	Asp	Trp	Pro	Phe	Asp	Asp	Gly	Thr	Ala	Pro	Ser	Ser	Gln	Ile
65					70					75				80	

Ile Asp Asn Trp Leu Lys Leu Met Lys Asn Lys Phe His Glu Asp Pro
 85 90 95
 Gly Cys Cys Ile Ala Ile His Cys Val Val Gly Phe Gly Xaa Ala Pro
 100 105 110
 Val Ala Ser Cys Pro Ser Phe Asn Xaa Arg Trp Asn Glu Ile Xaa Lys
 115 120 125
 Cys Ser Thr Val His Gln Ile Lys Val Thr Trp Asn Phe Xaa Gln Gln
 130 135 140
 Thr Thr Phe Val Phe Gly Glu Ile Leu Ser Xaa Asn Met Leu Ala Pro
 145 150 155 160
 Gln Lys Ser Gln Lys Xaa Leu Phe Pro Ser
 165 170

<210> 9
 <211> 1710
 <212> DNA
 <213> HOMO SAPIENS

<400> 9
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 gaggagctga aggaggtgag caaggagcag ccagactgg aggtgagta cctgccaac 120
 accaccaaga actgttaacc acatgtgcta cctatgacc actccagggt caggctgacc 180
 cagctggagg gagagcctca ttctgactac atcaatgcca acttggtccc aggtacacc 240
 cgcccacagg agttcattgc ctctcagggg cctctcaaga aaacactgga gaacttctgg 300
 cggctgggtgc gggagcagca ggtcgcate atcatcatgc cgaccatcag catggagaac 360
 gggaggggtgc tgtgtgagca ttactggctg accgactcta cccgggacac ccatggtcac 420
 atcaccatcc acctcctagc tgaggagcct gaggatgagt ggaccaagcg ggaattccag 480
 ctgcagcaag ttgtccagca acatcaacgg aggggtggagc aactgcagtt caccacctga 540
 tccgaccaca gcatacttga ggctcccagc tccctgctcg cctttatgga gctggtagag 600
 tagcaggcaa gggccaccca gggcgtggga cccatcctgg tgcactgcag gggtgtccc 660
 tgccgtgttg gcattgggac gacaggaacc ttctgtggcc tgtcagaggt gctgcagcag 720
 ctggaggagg agcagatggt agactgttcc catgctgtgt atgcactccg gatgcaccag 780
 cccctcatga tccagacct gagccagtag gtcttctctg acagctgctt actgaacaag 840
 attctggaag gaccttcaa catctctgag tcttggccca tctctgtgac ggacctcccg 900
 caggcgtgtg ccaagagggc agccagtgc aatgctggt tcttgaagga gtagaggcc 960
 atcaaggacg aggtctgctt ttccgcacc ccgcctggt atgagcagga cagccccgtc 1020

tectatgacc gttctaggg gcagttttct ccggtggagg agagccccc tgacgacatg 1080
 cctctctgga agccaatgat ctgtctctctg baggggtggc cctctgggag tgatcataag 1140
 gtgtgactg gccccgcagg gccaaaggag ctctggggag tgggtgtgga gcacaggggt 1200
 catgtgcttg tctctctttg ccacccaat gtcctggaga aggaattctg gccaacggag 1260
 atgagcccg tagtcacaga catgggtgag gtgcactggg tggctgagag cagcacagca 1320
 ggctgggttct gtacccctct caggggtcaca catggggaga gcaggaagga aaggagggtg 1380
 cagagactgc aatttcata cctggagcct gggcatgagc tgcccgccac caccctgctg 1440
 cccttctgg ctgctgtggg ccagtgtgc tctcggggca acaacaagaa gccgggcaca 1500
 ctgtcagcc actccaaaca ggggtcaacc cagctgggca ccttctggc catggagcag 1560
 ctgtcagc aggcagggtc tgagtgcacc gtggatatct ttaacgtggc cctgcagcag 1620
 tctcagggct gtggccttat gaccccaaca ctgaagcagt atgtctacct ctacaactgt 1680
 ctgaacagcg cgttggcaga cgggtgcgcc 1710

<210> 10
 <211> 570
 <212> PRT
 <213> HOMO SAPIENS

<220>
 <221> Variant
 <222> (46)..(46)
 <223> wherein 'Xaa' is any amino acid.

<220>
 <221> Variant
 <222> (180)..(180)
 <223> wherein 'Xaa' is any amino acid.

<220>
 <221> Variant
 <222> (201)..(201)
 <223> wherein 'Xaa' is any amino acid.

<400> 10

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 1 5 10 15

Phe Leu Lys Phe Glu Glu Leu Lys Glu Val Ser Lys Glu Gln Pro Arg
 20 25 30

Leu Glu Ala Glu Tyr Pro Ala Asn Thr Thr Lys Asn Cys Xaa Pro His
 35 40 45
 Val Leu Pro Tyr Asp His Ser Arg Val Arg Leu Thr Gln Leu Glu Gly
 50 55 60
 Glu Pro His Ser Asp Tyr Ile Asn Ala Asn Leu Val Pro Gly Tyr Thr
 65 70 75 80
 Arg Pro Gln Glu Phe Ile Ala Ser Gln Gly Pro Leu Lys Lys Thr Leu
 85 90 95
 Glu Asn Phe Trp Arg Leu Val Arg Glu Gln Gln Val Arg Ile Ile Ile
 100 105 110
 Met Pro Thr Ile Ser Met Glu Asn Gly Arg Val Leu Cys Glu His Tyr
 115 120 125
 Trp Leu Thr Asp Ser Thr Pro Asp Thr His Gly His Ile Thr Ile His
 130 135 140
 Leu Leu Ala Glu Glu Pro Glu Asp Glu Trp Thr Lys Arg Glu Phe Gln
 145 150 155 160
 Leu Gln His Val Val Gln Gln His Gln Arg Arg Val Glu Gln Leu Gln
 165 170 175
 Phe Thr Thr Xaa Ser Asp His Ser Ile Leu Glu Ala Pro Ser Ser Leu
 180 185 190
 Leu Ala Phe Met Glu Leu Val Gln Xaa Gln Ala Arg Ala Thr Gln Gly
 195 200 205
 Val Gly Pro Ile Leu Val His Cys Arg Gly Cys Pro Cys Gly Val Gly
 210 215 220
 Met Gly Arg Thr Gly Thr Phe Val Ala Leu Ser Arg Leu Leu Gln Gln
 225 230 235 240
 Leu Glu Glu Glu Gln Met Val Asp Val Phe His Ala Val Tyr Ala Leu
 245 250 255
 Arg Met His Gln Pro Leu Met Ile Gln Thr Leu Ser Gln Tyr Val Phe
 260 265 270
 Leu His Ser Cys Leu Leu Asn Lys Ile Leu Glu Gly Pro Phe Asn Ile
 275 280 285
 Ser Glu Ser Trp Pro Ile Ser Val Thr Asp Leu Pro Gln Ala Cys Ala
 290 295 300
 Lys Arg Ala Ala Ser Ala Asn Ala Gly Phe Leu Lys Glu Tyr Glu Ala
 305 310 315 320
 Ile Lys Asp Glu Ala Gly Phe Ser Ala Pro Pro Pro Gly Tyr Glu Gln
 325 330 335

Asp Ser Pro Val Ser Tyr Asp Arg Ser Gln Gly Gln Phe Ser Pro Val
 340 345 350
 Glu Glu Ser Pro Pro Asp Asp Met Pro Leu Trp Lys Pro Met Ile Cys
 355 360 365
 Ala Leu Gln Gly Gly Pro Ser Gly Arg Asp His Thr Val Leu Thr Gly
 370 375 380
 Pro Ala Gly Pro Lys Glu Leu Trp Glu Leu Val Trp Gln His Arg Ala
 385 390 395 400
 His Val Leu Val Ser Leu Cys Pro Pro Asn Val Met Glu Lys Glu Phe
 405 410 415
 Trp Pro Thr Glu Met Gln Pro Val Val Thr Asp Met Val Thr Val His
 420 425 430
 Trp Val Ala Glu Ser Ser Thr Ala Gly Trp Phe Cys Thr Leu Leu Arg
 435 440 445
 Val Thr His Gly Glu Ser Arg Lys Glu Arg Glu Val Gln Arg Leu Gln
 450 455 460
 Phe Pro Tyr Leu Glu Pro Gly His Glu Leu Pro Ala Thr Thr Leu Leu
 465 470 475 480
 Pro Phe Leu Ala Ala Val Gly Gln Cys Cys Ser Arg Gly Asn Asn Lys
 485 490 495
 Lys Pro Gly Thr Leu Leu Ser His Ser Asn Lys Gly Ala Thr Gln Leu
 500 505 510
 Gly Thr Phe Leu Ala Met Glu Gln Leu Leu Gln Gln Ala Gly Ser Glu
 515 520 525
 Cys Thr Val Asp Ile Phe Asn Val Ala Leu Gln Gln Ser Gln Ala Cys
 530 535 540
 Gly Leu Met Thr Pro Thr Leu Lys Gln Tyr Val Tyr Leu Tyr Asn Cys
 545 550 555 560
 Leu Asn Ser Ala Leu Ala Asp Gly Leu Pro
 565 570

<210> 11

<211> 63

<212> DNA

<213> HOMO SAPIENS

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60

gag

63

<210> 12

<211> 91
 <212> DNA
 <213> HOMO SAPIENS

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 appaagaatt gttaaccaca tgtgctaccc t 91

<210> 13
 <211> 77
 <212> DNA
 <213> HOMO SAPIENS

<400> 13
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 atgccaactt ggcccc 77

<210> 14
 <211> 135
 <212> DNA
 <213> HOMO SAPIENS

<400> 14
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 aactcttggc ggctgggtgcg ggagcagcag gtccgcacaa tcatcatgcc gaccatcagc 120
 atggagaang ggagg 135

<210> 15
 <211> 123
 <212> DNA
 <213> HOMO SAPIENS

<400> 15
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 atccaccttc tagctgagga gcttgaggat gactggacca agcgggaatt ccagctgcag 120
 cac 123

<210> 17
 <211> 141
 <212> DNA
 <213> HOMO SAPIENS

<400> 18
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 agcatccttg aggtccccag ctccctgctc gcttttatgg agctgggtaca gtagcaggca 120

aggagcaacc agggcggtggg acccatcctg gtgcactgca g 151

<210> 17
 <211> 151
 <212> DNA
 <213> HOMO SAPIENS

<400> 17
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 gctgagagag ctggaggagg agcagatggt agacgtgttc catgtgtgt atgcactccg 120
 gatgcaccag cccctcatga tccagaccct g 151

<210> 18
 <211> 68
 <212> DNA
 <213> HOMO SAPIENS

<400> 18
 agccagtaag tcttctcgca cagctgcta ctgaacaaga ttctggaagg acccttcaac 50
 atctctga 68

<210> 19
 <211> 88
 <212> DNA
 <213> HOMO SAPIENS

<400> 19
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 caatgctggc ttcttgaagg agtacgag 88

<210> 20
 <211> 67
 <212> DNA
 <213> HOMO SAPIENS

<400> 20
 gccatcaagg acgaggctgg cttttccgca cccccgctg gctatgagca ggacagcccc 50
 gtctcct 67

<210> 21
 <211> 58
 <212> DNA
 <213> HOMO SAPIENS

<400> 21
 atgacgttc tcaggggcag ttttctccgg tggaggagag cccccctgac gacatgcc 58

<210> 22
 <211> 160
 <212> DNA
 <213> HOMO SAPIENS

<400> 22
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 gctgactggc cccgcagggc caaaggagct ctgggagctg gtgtggcagc acagggctca 120
 tgtgcttctc tctctttggc caccacaatgt catggagaag 150

<210> 23
 <211> 111
 <212> DNA
 <213> HOMO SAPIENS

<400> 23
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 gctgagagca gcacagcagg ctgggtctct accctctca gggtcacaca t 111

<210> 24
 <211> 164
 <212> DNA
 <213> HOMO SAPIENS

<400> 24
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 catgagctgc ccgccaccac cctgctgccc ttctggctg ctgtgggcca gtgctgctct 120
 cgggagcaaca acaagaagcc gggcacactg ctacgccact ccaa 164

<210> 25
 <211> 136
 <212> DNA
 <213> HOMO SAPIENS

<400> 25
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 tatgaccaca acactg 136

<210> 26
 <211> 57
 <212> RNA
 <213> HOMO SAPIENS

<400> 26

Asp Thr Ile Gly Lys Glu Lys Leu Phe His Phe Thr Glu Glu Thr Pro
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 275 280 285
 Ser Asp Tyr Glu Thr Thr Ser Gln Pro Tyr Trp Trp Asp Ser Ala Ser
 290 295 300
 Ala Ala Pro Glu Ser Glu Asp Glu Phe Val Ser Val Leu Pro Met Glu
 305 310 315 320
 Tyr Glu Asn Asn Ser Thr Leu Ser Glu Thr Glu Lys Ser Thr Ser Gly
 325 330 335
 Ser Phe Ser Phe Phe Pro Val Gln Met Ile Leu Thr Trp Leu Pro Pro
 340 345 350
 Lys Pro Pro Thr Ala Phe Asp Gly Phe His Ile His Ile Glu Arg Glu
 355 360 365
 Glu Asn Phe Thr Glu Tyr Leu Met Val Asp Glu Glu Ala His Glu Phe
 370 375 380
 Val Ala Glu Leu Lys Glu Pro Gly Lys Tyr Lys Leu Ser Val Thr Thr
 385 390 395 400
 Phe Ser Ser Ser Gly Ser Cys Glu Thr Arg Lys Ser Gln Ser Ala Lys
 405 410 415
 Ser Leu Ser Phe Tyr Ile Ser Pro Ser Gly Glu Trp Ile Glu Glu Leu
 420 425 430
 Thr Glu Lys Pro Gln His Val Ser Val His Val Leu Ser Ser Thr Thr
 435 440 445
 Ala Leu Met Ser Trp Thr Ser Ser Gln Glu Asn Tyr Asn Ser Thr Ile
 450 455 460
 Val Ser Val Val Ser Leu Thr Cys Gln Lys Gln Lys Glu Ser Gln Arg
 465 470 475 480
 Leu Glu Lys Gln Tyr Cys Thr Gln Val Asn Ser Ser Lys Pro Ile Ile
 485 490 495
 Glu Asn Leu Val Pro Gly Ala Gln Tyr Gln Val Val Ile Tyr Leu Arg
 500 505 510
 Lys Gly Pro Leu Ile Gly Pro Pro Ser Asp Pro Val Thr Phe Ala Ile
 515 520 525
 Val Pro Thr Gly Ile Lys Asp Leu Met Leu Tyr Pro Leu Gly Pro Thr
 530 535 540
 Ala Val Val Leu Ser Trp Thr Arg Pro Tyr Leu Gly Val Phe Arg Lys
 545 550 555 560

Tyr	Val	Val	Glu	Met	Phe	Tyr	Phe	Asn	Pro	Ala	Thr	Met	Thr	Ser	Glu	
				555					570					575		
Trp	Thr	Thr	Tyr	Tyr	Glu	Ile	Ala	Ala	Thr	Val	Ser	Leu	Thr	Ala	Ser	
			580					585					590			
Val	Arg	Ile	Ala	Asn	Leu	Leu	Pro	Ala	Trp	Tyr	Tyr	Asn	Phe	Arg	Val	
		595					600					605				
Thr	Met	Val	Thr	Trp	Gly	Asp	Pro	Glu	Leu	Ser	Cys	Cys	Asp	Ser	Ser	
	610					615					620					
Thr	Ile	Ser	Phe	Ile	Thr	Ala	Pro	Val	Ala	Pro	Glu	Ile	Thr	Ser	Val	
	625				630					635					640	
Glu	Tyr	Phe	Asn	Ser	Leu	Leu	Tyr	Ile	Ser	Trp	Thr	Tyr	Gly	Asp	Asp	
			645						650					655		
Thr	Thr	Asp	Leu	Ser	His	Ser	Arg	Met	Leu	His	Trp	Met	Val	Val	Ala	
		660						665					670			
Glu	Gly	Lys	Lys	Lys	Ile	Lys	Lys	Ser	Val	Thr	Arg	Asn	Val	Met	Thr	
		675					680					685				
Ala	Ile	Leu	Ser	Leu	Pro	Pro	Gly	Asp	Ile	Tyr	Asn	Leu	Ser	Val	Thr	
	690					695					700					
Ala	Cys	Thr	Glu	Arg	Gly	Ser	Asn	Thr	Ser	Met	Leu	Arg	Leu	Val	Lys	
	705				710					715					720	
Leu	Glu	Pro	Ala	Pro	Pro	Lys	Ser	Leu	Phe	Ala	Val	Asn	Lys	Thr	Gln	
			725						730					735		
Thr	Ser	Val	Thr	Leu	Leu	Trp	Val	Glu	Glu	Gly	Val	Ala	Asp	Phe	Phe	
			740					745					750			
Glu	Val	Phe	Cys	Gln	Gln	Val	Gly	Ser	Ser	Gln	Lys	Thr	Lys	Leu	Gln	
		755					760					765				
Glu	Pro	Val	Ala	Val	Ser	Ser	His	Val	Val	Thr	Ile	Ser	Ser	Leu	Leu	
	770					775					780					
Pro	Ala	Thr	Ala	Tyr	Asn	Cys	Ser	Val	Thr	Ser	Phe	Ser	His	Asp	Ser	
	785				790					795					800	
Pro	Ser	Val	Pro	Thr	Phe	Ile	Ala	Val	Ser	Thr	Met	Val	Thr	Glu	Met	
			805						810					815		
Asn	Pro	Asn	Val	Val	Val	Ile	Ser	Val	Leu	Ala	Ile	Leu	Ser	Thr	Leu	
			820						825				830			
Leu	Ile	Gly	Leu	Leu	Leu	Val	Thr	Leu	Ile	Ile	Leu	Arg	Lys	Lys	His	
		835					840					845				
Leu	Gln	Met	Ala	Arg	Glu	Cys	Gly	Ala	Gly	Thr	Phe	Val	Asn	Phe	Ala	
	850					855					860					

Ser Leu Glu Arg Asp Gly Lys Leu Pro Tyr Asn Trp Ser Lys Asn Gly
 865 870 875 880
 Leu Lys Lys Arg Lys Leu Thr Asn Pro Val Gln Leu Asp Asp Phe Asp
 885 890 895
 Ala Tyr Ile Lys Asp Met Ala Lys Asp Ser Asp Tyr Lys Phe Ser Leu
 900 905 910
 Gln Phe Glu Glu Leu Lys Leu Ile Gly Leu Asp Ile Pro His Phe Ala
 915 920 925
 Ala Asp Leu Pro Leu Asn Arg Cys Lys Asn Arg Tyr Thr Asn Ile Leu
 930 935 940
 Pro Tyr Asp Phe Ser Arg Val Arg Leu Val Ser Met Asn Glu Glu Glu
 945 950 955 960
 Gly Ala Asp Tyr Ile Asn Ala Asn Tyr Ile Pro Gly Tyr Asn Ser Pro
 965 970 975
 Gln Glu Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Arg Asn Asp
 980 985 990
 Phe Trp Lys Met Val Leu Gln Gln Lys Ser Gln Ile Ile Val Met Leu
 995 1000 1005
 Thr Gln Cys Asn Glu Lys Arg Arg Val Lys Cys Asp His Tyr Trp
 1010 1015 1020
 Pro Phe Thr Glu Glu Pro Ile Ala Tyr Gly Asp Ile Thr Val Glu
 1025 1030 1035
 Met Ile Ser Glu Glu Glu Gln Asp Asp Trp Ala Cys Arg His Phe
 1040 1045 1050
 Arg Ile Asn Tyr Ala Asp Glu Met Gln Asp Val Met His Phe Asn
 1055 1060 1065
 Tyr Thr Ala Trp Pro Asp His Gly Val Pro Thr Ala Asn Ala Ala
 1070 1075 1080
 Glu Ser Ile Leu Gln Phe Val His Met Val Arg Gln Gln Ala Thr
 1085 1090 1095
 Lys Ser Lys Gly Pro Met Ile Ile His Cys Ser Ala Gly Val Gly
 1100 1105 1110
 Arg Thr Gly Thr Phe Ile Ala Leu Asp Arg Leu Leu Gln His Ile
 1115 1120 1125
 Arg Asp His Glu Phe Val Asp Ile Leu Gly Leu Val Ser Glu Met
 1130 1135 1140
 Arg Ser Tyr Arg Met Ser Met Val Gln Thr Glu Glu Gln Tyr Ile
 1145 1150 1155

Phe Ile His Gln Cys Val Gln Leu Met Trp Met Lys Lys Lys Gln
 1160 1165 1170

Gln Phe Cys Ile Ser Asp Val Ile Tyr Glu Asn Val Ser Lys Ser
 1175 1180 1185

<010> 28
 <011> 405
 <012> PRT
 <013> Mus musculus

<400> 28

Met Val Thr Glu Val Asn Pro Asn Val Val Val Ile Ser Val Leu Ala
 1 5 10 15

Ile Leu Ser Thr Leu Leu Ile Gly Leu Leu Leu Val Thr Leu Val Ile
 20 25 30

Leu Arg Lys Lys His Leu Gln Met Ala Arg Glu Cys Gly Ala Gly Thr
 35 40 45

Phe Val Asn Phe Ala Ser Leu Glu Arg Glu Gly Lys Leu Pro Tyr Ser
 50 55 60

Trp Arg Arg Ser Val Phe Ala Leu Leu Thr Leu Leu Pro Ser Cys Leu
 65 70 75 80

Trp Thr Asp Tyr Leu Leu Ala Phe Tyr Ile Asn Pro Trp Ser Lys Asn
 85 90 95

Gly Leu Lys Lys Arg Lys Leu Thr Asn Pro Val Glu Leu Asp Asp Phe
 100 105 110

Asp Ser Tyr Ile Lys Asp Met Ala Lys Asp Ser Asp Tyr Lys Phe Ser
 115 120 125

Leu Gln Phe Glu Glu Leu Lys Leu Ile Gly Leu Asp Ile Pro His Phe
 130 135 140

Ala Ala Asp Leu Pro Leu Asn Arg Cys Lys Asn Arg Tyr Thr Asn Ile
 145 150 155 160

Leu Pro Tyr Asp Phe Ser Arg Val Arg Leu Val Ser Met Asn Glu Glu
 165 170 175

Glu Gly Ala Asp Tyr Ile Asn Ala Asn Tyr Ile Pro Gly Tyr Asn Ser
 180 185 190

Pro Gln Glu Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Arg Asn
 195 200 205

Asp Phe Trp Lys Met Val Leu Gln Gln Lys Ser His Ile Ile Val Met
 210 215 220

Leu Thr Gln Cys Asn Glu Lys Arg Arg Val Lys Cys Asp His Tyr Trp

225		230		235		240
Pro Phe Thr Glu Glu	Pro Ile Ala Tyr Gly	Asp Ile Thr Val Glu	Met			
	245		250		255	
Val Ser Glu Glu Glu Glu	Asp Trp Ala Ser Arg His	Phe Arg Ile				
	260	265		270		
Asn Tyr Ala Asp Glu Ala	Gln Asp Val Met His	Phe Asn Tyr Thr Gly				
	275	280	285			
Trp Pro Asp His Gly Val	Pro Pro Ala Asn Ala	Ala Glu Ser Ile Leu				
	290	295	300			
Gln Phe Val Phe Thr Val	Arg Gln Gln Ala Ala	Lys Ser Lys Gly Pro				
	305	310	315			320
Met Ile Ile His Cys Ser	Ala Gly Val Gly Arg Thr	Gly Thr Phe Ile				
	325	330	335			
Ala Leu Asp Arg Leu Leu	Gln His Ile Arg Asp His	Glu Phe Val Asp				
	340	345	350			
Ile Leu Gly Leu Val Ser	Glu Met Arg Ser Tyr Arg	Met Ser Met Val				
	355	360	365			
Gln Thr Glu Glu Gln Tyr	Ile Phe Ile His Gln Cys	Val Gln Leu Met				
	370	375	380			
Trp Leu Arg Lys Lys Gln	Gln Phe Cys Ile Ser Asp	Val Ile Tyr Glu				
	385	390	395		400	
Asn Val Ser Lys Ser						
	405					

<210> 29
 <211> 303
 <212> PRT
 <213> Schizosaccharomyces pombe

 <400> 29

Met Ser Phe Lys Glu Val	Ser Thr Glu Asn Gly Val	Leu Thr Pro Leu
1	5	10 15
Ile Thr Ile Lys Glu Lys	Ala Tyr Met Ile Ile Glu Gly	Leu Asn Glu
	20	25 30
Glu Glu Ile Glu Leu Leu	Asn Thr Arg Leu Pro Lys	Leu Ser Lys Lys
	35	40 45
Ala Leu Ala Arg Asn Arg	Tyr Ser Asn Ile Val Pro Tyr	Glu Asn Thr
	50	55 60
Arg Val Arg Leu Asp	Pro Met Trp Lys Glu Ala	Cys Asp Tyr Ile Asn
	65	70 75 80

Ala Ser Ile Val Lys Ile Pro Ser Gly Lys Thr Phe Ile Ala Thr Gln
 85 90 95
 Gly Pro Thr Ser Asn Ser Ile Asp Val Phe Trp Lys Met Val Trp Gln
 100 105 110
 Ser Val Pro Lys Ser Gly Ile Ile Val Met Leu Thr Lys Leu Arg Glu
 115 120 125
 Arg His Arg Leu Lys Cys Asp Ile Tyr Trp Pro Val Glu Leu Phe Glu
 130 135 140
 Thr Leu Asn Ile Gly Asp Leu Ser Val Ile Leu Val Lys Val Tyr Thr
 145 150 155 160
 Leu Thr Ser Leu Asn Glu Val Gln Val Arg Glu Phe Glu Leu Asn Lys
 165 170 175
 Asp Gly Val Lys Lys Lys Ile Leu His Phe Tyr Tyr Asn Gly Trp Pro
 180 185 190
 Asp Phe Gly Ala Pro His Thr Phe Ser Leu Leu Ser Leu Thr Arg Tyr
 195 200 205
 Ile Lys Ser Leu Ser Tyr Ser Pro Asp Phe Glu Thr Ala Pro Ile Ile
 210 215 220
 Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Thr Phe Met Ala Leu
 225 230 235 240
 Phe Glu Ile Leu Ser Gln Thr Asp Asp Ser Thr Ser Thr Ser Lys Phe
 245 250 255
 Glu Val Asp Asn Ile Ala Asn Ile Val Ser Ser Leu Arg Ser Gln Arg
 260 265 270
 Met Gln Ser Val Gln Ser Val Asp Gln Leu Val Phe Leu Tyr Thr Val
 275 280 285
 Ser Gln Glu Leu Leu Gln Gly Lys Glu Phe Leu Leu Pro Gln Leu
 290 295 300

<210> 30
 <211> 580
 <212> PRT
 <213> homo sapiens

<400> 30

Met Lys Asp Arg Leu Tyr Phe Ala Thr Leu Arg Asn Arg Pro Lys Ser
 1 5 10 15
 Thr Val Asn Thr His Tyr Phe Ser Ile Asp Glu Glu Leu Val Tyr Glu
 20 25 30
 Asn Phe Tyr Ala Asp Phe Gly Pro Leu Asn Leu Ala Met Val Tyr Arg
 35 40 45

Tyr	Cys	Cys	Lys	Leu	Asn	Lys	Lys	Leu	Lys	Ser	Tyr	Ser	Leu	Ser	Arg	
50						55					60					
Lys	Lys	Ile	Val	His	Tyr	Thr	Cys	Phe	Asp	Gln	Arg	Lys	Arg	Ala	Asn	
65					70				75						80	
Ala	Ala	Phe	Leu	Ile	Gly	Ala	Tyr	Ala	Val	Ile	Tyr	Leu	Lys	Lys	Thr	
			85						90					95		
Pro	Glu	Glu	Ala	Tyr	Arg	Ala	Leu	Leu	Ser	Gly	Ser	Asn	Pro	Pro	Tyr	
			100					105					110			
Leu	Pro	Phe	Arg	Asp	Ala	Ser	Phe	Gly	Asn	Cys	Thr	Tyr	Asn	Leu	Thr	
		115					120					125				
Ile	Leu	Asp	Cys	Leu	Gln	Gly	Ile	Arg	Lys	Gly	Leu	Gln	His	Gly	Phe	
130						135					140					
Phe	Asp	Phe	Glu	Thr	Ile	Asp	Val	Asp	Glu	Tyr	Glu	His	Tyr	Glu	Arg	
145					150					155					160	
Val	Glu	Asn	Gly	Asp	Phe	Asn	Cys	Ile	Val	Pro	Gly	Lys	Phe	Leu	Ala	
			165						170					175		
Phe	Ser	Gly	Pro	His	Pro	Lys	Ser	Lys	Ile	Glu	Asn	Gly	Tyr	Pro	Leu	
			180					185					190			
His	Ala	Pro	Glu	Ala	Tyr	Phe	Pro	Tyr	Phe	Lys	Lys	His	Asn	Val	Thr	
		195					200						205			
Ala	Val	Val	Arg	Leu	Asn	Lys	Lys	Ile	Tyr	Glu	Ala	Lys	Arg	Phe	Thr	
210						215					220					
Asp	Ala	Gly	Phe	Glu	His	Tyr	Asp	Leu	Phe	Phe	Ile	Asp	Gly	Ser	Thr	
225					230					235					240	
Pro	Ser	Asp	Asn	Ile	Val	Arg	Arg	Phe	Leu	Asn	Ile	Cys	Glu	Asn	Thr	
			245						250					255		
Glu	Gly	Ala	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu	Gly	Arg	Thr	Gly	
			260					265					270			
Thr	Leu	Ile	Ala	Cys	Tyr	Val	Met	Lys	His	Tyr	Arg	Phe	Thr	His	Ala	
		275					280					285				
Glu	Ile	Ile	Ala	Trp	Ile	Arg	Ile	Cys	Arg	Pro	Gly	Ser	Ile	Ile	Gly	
290					295						300					
Pro	Gln	Gln	His	Phe	Leu	Glu	Glu	Lys	Gln	Ala	Ser	Leu	Trp	Val	Gln	
305					310					315					320	
Gly	Asp	Ile	Phe	Arg	Ser	Lys	Leu	Lys	Asn	Arg	Pro	Ser	Ser	Glu	Gly	
			325						330					335		
Ser	Ile	Asn	Lys	Ile	Leu	Ser	Gly	Leu	Asp	Asp	Met	Ser	Ile	Gly	Gly	
		340						345					350			

Asn Leu Ser Lys Thr Gln Asn Met Glu Arg Phe Gly Glu Asp Asn Leu
355 360 365

Glu Asp Asp Asp Val Glu Met Lys Asn Gly Ile Thr Gln Gly Asp Lys
370 375 380

Leu Arg Ala Leu Lys Ser Gln Arg Gln Pro Arg Thr Ser Pro Ser Cys
385 390 395 400

Ala Phe Arg Ser Asp Asp Thr Lys Gly His Pro Arg Ala Val Ser Gln
405 410 415

Pro Phe Arg Leu Ser Ser Ser Leu Gln Gly Ser Ala Val Thr Leu Lys
420 425 430

Thr Ser Lys Met Ala Leu Ser Pro Ser Ala Thr Ala Lys Arg Ile Asn
435 440 445

Arg Thr Ser Leu Ser Ser Gly Ala Thr Val Arg Ser Phe Ser Ile Asn
450 455 460

Ser Arg Leu Ala Ser Ser Leu Gly Asn Leu Asn Ala Ala Thr Asp Asp
465 470 475 480

Pro Glu Asn Lys Lys Thr Ser Ser Ser Ser Lys Ala Gly Phe Thr Ala
485 490 495

Ser Pro Phe Thr Asn Leu Leu Asn Gly Ser Ser Gln Pro Thr Thr Arg
500 505 510

Asn Tyr Pro Glu Leu Asn Asn Asn Gln Tyr Asn Arg Ser Ser Asn Ser
515 520 525

Asn Gly Gly Asn Leu Asn Ser Pro Pro Gly Pro His Ser Ala Lys Thr
530 535 540

Glu Glu His Thr Thr Ile Leu Arg Pro Ser Tyr Thr Gly Leu Ser Ser
545 550 555 560

Ser Ser Ala Arg Phe Leu Ser Arg Ser Ile Pro Ser Leu Gln Ser Glu
565 570 575

Tyr Val His Tyr
580

<210> 31
<211> 459
<212> PRT
<213> homo sapiens

<400> 31

Met Lys Arg Lys Ser Glu Arg Arg Ser Ser Trp Ala Ala Ala Pro Pro
1 5 10 15

Cys Ser Arg Arg Cys Ser Ser Thr Ser Pro Gly Val Lys Lys Ile Arg

20					25					30					
Ser	Ser	Thr	Gln	Gln	Asp	Pro	Arg	Arg	Arg	Asp	Pro	Gln	Asp	Asp	Val
		35					40					45			
Tyr	Leu	Asp	Ile	Thr	Asp	Arg	Leu	Cys	Phe	Ala	Ile	Leu	Tyr	Ser	Arg
	50					55					60				
Pro	Lys	Ser	Ala	Ser	Asn	Val	His	Tyr	Phe	Ser	Ile	Asp	Asn	Glu	Leu
65					70					75				80	
Glu	Tyr	Glu	Asn	Phe	Tyr	Ala	Asp	Phe	Gly	Pro	Leu	Asn	Leu	Ala	Met
			85						90					95	
Val	Tyr	Arg	Tyr	Cys	Cys	Lys	Ile	Asn	Lys	Lys	Leu	Lys	Ser	Ile	Thr
			100					105					110		
Met	Leu	Arg	Lys	Lys	Ile	Val	His	Phe	Thr	Gly	Ser	Asp	Gln	Arg	Lys
	115						120					125			
Gln	Ala	Asn	Ala	Ala	Phe	Leu	Val	Gly	Cys	Tyr	Met	Val	Ile	Tyr	Leu
	130					135					140				
Gly	Arg	Thr	Pro	Glu	Glu	Ala	Tyr	Arg	Ile	Leu	Ile	Phe	Gly	Glu	Thr
145					150					155				160	
Ser	Tyr	Ile	Pro	Phe	Arg	Asp	Ala	Ala	Tyr	Gly	Ser	Cys	Asn	Phe	Tyr
				165					170					175	
Ile	Thr	Leu	Leu	Asp	Cys	Phe	His	Ala	Val	Lys	Lys	Ala	Met	Gln	Tyr
		180					185						190		
Gly	Phe	Leu	Asn	Phe	Asn	Ser	Phe	Asn	Leu	Asp	Glu	Tyr	Glu	His	Tyr
	195						200					205			
Glu	Lys	Ala	Glu	Asn	Gly	Asp	Leu	Asn	Trp	Ile	Ile	Pro	Asp	Arg	Phe
	210					215					220				
Ile	Ala	Phe	Cys	Gly	Pro	His	Ser	Arg	Ala	Arg	Leu	Glu	Ser	Gly	Tyr
225					230				235					240	
His	Gln	His	Ser	Pro	Glu	Thr	Tyr	Ile	Gln	Tyr	Phe	Lys	Asn	His	Asn
				245					250					255	
Val	Thr	Thr	Ile	Ile	Arg	Leu	Asn	Lys	Arg	Met	Tyr	Asp	Ala	Lys	Arg
			260					265					270		
Phe	Thr	Asp	Ala	Gly	Phe	Asp	His	His	Asp	Leu	Phe	Phe	Ala	Asp	Gly
		275					280					285			
Ser	Thr	Pro	Thr	Asp	Ala	Ile	Val	Lys	Glu	Phe	Leu	Asp	Ile	Cys	Glu
	290					295					300				
Asn	Ala	Glu	Gly	Ala	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu	Gly	Arg
305				310					315					320	
Thr	Gly	Thr	Leu	Ile	Ala	Cys	Tyr	Ile	Met	Lys	His	Tyr	Arg	Met	Thr

325	330	335
Ala Ala Glu Thr Ile Ala Trp Val Arg Ile Cys Arg Pro Gly Ser Val 340	345	350
Ile Gly Pro Gln Gln Gln Phe Leu Val Met Lys Gln Thr Asn Leu Trp 355	360	365
Leu Glu Gly Asp Tyr Phe Arg Gln Lys Leu Lys Gly Gln Glu Asn Gly 370	375	380
Gln His Arg Ala Ala Phe Ser Lys Leu Leu Ser Gly Val Asp Asp Ile 385	390	395
Ser Ile Asn Gly Val Glu Asn Gln Asp Gln Gln Glu Pro Glu Pro Tyr 405	410	415
Ser Asp Asp Asp Glu Ile Asn Gly Val Thr Gln Gly Asp Arg Leu Arg 420	425	430
Ala Leu Lys Ser Arg Arg Gln Ser Lys Thr Asn Ala Ile Pro Leu Thr 435	440	445
Leu Ser Ile Ser Arg Thr Lys Thr Val Leu Arg 450	455	
<210> 32		
<211> 551		
<212> PFT		
<213> Saccharomyces cerevisiae		
<400> 32		
Met Arg Arg Ser Val Tyr Leu Asp Asn Thr Ile Glu Phe Leu Arg Gly 1	5	10
Arg Val Tyr Leu Gly Ala Tyr Asp Tyr Thr Pro Glu Asp Thr Asp Glu 20	25	30
Leu Val Phe Phe Thr Val Glu Asp Ala Ile Phe Tyr Asn Ser Phe His 35	40	45
Leu Asp Phe Gly Pro Met Asn Ile Gly His Leu Tyr Arg Phe Ala Val 50	55	60
Ile Phe His Glu Ile Leu Asn Asp Pro Glu Asn Ala Asn Lys Ala Val 65	70	75
Val Phe Tyr Ser Ser Ala Ser Thr Arg Gln Arg Ala Asn Ala Ala Cys 85	90	95
Met Leu Cys Cys Tyr Met Ile Leu Val Gln Ala Trp Thr Pro His Gln 100	105	110
Val Leu Gln Pro Leu Ala Gln Val Asp Pro Pro Phe Met Pro Phe Arg 115	120	125

Asp	Ala	Gly	Tyr	Ser	Asn	Ala	Asp	Phe	Glu	Ile	Thr	Ile	Gln	Asp	Val	130	135	140
Val	Tyr	Gly	Val	Trp	Arg	Ala	Lys	Glu	Lys	Gly	Leu	Ile	Asp	Leu	His	145	150	155
Ser	Phe	Asn	Leu	Glu	Ser	Tyr	Glu	Lys	Tyr	Glu	His	Val	Glu	Phe	Gly	165	170	175
Asp	Phe	Asn	Val	Leu	Thr	Pro	Asp	Phe	Ile	Ala	Phe	Ala	Ser	Pro	Gln	180	185	190
Glu	Asp	His	Pro	Lys	Gly	Tyr	Leu	Ala	Thr	Lys	Ser	Ser	His	Leu	Asn	195	200	205
Gln	Pro	Phe	Lys	Ser	Val	Leu	Asn	Phe	Phe	Ala	Asn	Asn	Asn	Val	Gln	210	215	220
Leu	Val	Val	Arg	Leu	Asn	Ser	His	Leu	Tyr	Asn	Lys	Lys	His	Phe	Glu	225	230	235
Asp	Ile	Gly	Ile	Gln	His	Leu	Asp	Leu	Ile	Phe	Glu	Asp	Gly	Thr	Cys	245	250	255
Pro	Asp	Leu	Ser	Ile	Val	Lys	Asn	Phe	Val	Gly	Ala	Ala	Glu	Thr	Ile	260	265	270
Ile	Lys	Arg	Gly	Gly	Lys	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu	Gly	275	280	285
Arg	Thr	Gly	Cys	Leu	Ile	Gly	Ala	His	Leu	Ile	Tyr	Thr	Tyr	Gly	Phe	290	295	300
Thr	Ala	Asn	Glu	Cys	Ile	Gly	Phe	Leu	Arg	Phe	Ile	Arg	Pro	Gly	Met	305	310	315
Val	Val	Gly	Pro	Gln	Gln	His	Trp	Leu	Tyr	Leu	His	Gln	Asn	Asp	Phe	325	330	335
Arg	Glu	Trp	Lys	Tyr	Thr	Thr	Arg	Ile	Ser	Leu	Lys	Pro	Ser	Glu	Ala	340	345	350
Ile	Gly	Gly	Leu	Tyr	Pro	Leu	Ile	Ser	Leu	Glu	Glu	Tyr	Arg	Leu	Gln	355	360	365
Lys	Lys	Lys	Leu	Lys	Asp	Asp	Lys	Arg	Val	Ala	Gln	Asn	Asn	Ile	Glu	370	375	380
Gly	Glu	Leu	Arg	Asp	Leu	Thr	Met	Thr	Pro	Pro	Ser	Asn	Gly	His	Gly	385	390	395
Ala	Leu	Ser	Ala	Arg	Asn	Ser	Ser	Gln	Pro	Ser	Thr	Ala	Asn	Asn	Gly	405	410	415
Ser	Asn	Ser	Phe	Lys	Ser	Ser	Ala	Val	Pro	Gln	Thr	Ser	Pro	Gly	Gln	420	425	430

Pro Arg Lys Gly Gln Asn Gly Ser Asn Thr Ile Glu Asp Ile Asn Asn
 435 440 445

Asn Arg Asn Pro Thr Ser His Ala Asn Arg Lys Val Val Ile Glu Ser
 450 455 460

Asn Asn Ser Asp Asp Glu Ser Met Gln Asp Thr Asn Gly Thr Ser Asn
 465 470 475 480

His Tyr Pro Lys Val Ser Arg Lys Lys Asn Asp Ile Ser Ser Ala Ser
 485 490 495

Ser Ser Arg Met Glu Asp Asn Glu Pro Ser Ala Thr Asn Ile Asn Asn
 500 505 510

Ala Ala Asp Asp Thr Ile Leu Arg Gln Leu Leu Pro Lys Asn Arg Arg
 515 520 525

Val Thr Ser Gly Arg Arg Thr Thr Ser Ala Ala Gly Gly Ile Arg Lys
 530 535 540

Ile Ser Gly Ser Ile Lys Lys
 545 550

<210> 33

<211> 173

<212> PRT

<213> homo sapiens

<400> 33

Met Ala Arg Met Asn Arg Pro Ala Pro Val Glu Val Thr Tyr Lys Asn
 1 5 10 15

Met Arg Phe Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys
 20 25 30

Phe Ile Glu Glu Leu Lys Lys Tyr Gly Val Thr Thr Ile Val Arg Val
 35 40 45

Cys Glu Ala Thr Tyr Asp Thr Thr Leu Val Glu Lys Glu Gly Ile His
 50 55 60

Val Leu Asp Trp Pro Phe Asp Asp Gly Ala Pro Pro Ser Asn Gln Ile
 65 70 75 80

Val Asp Asp Trp Leu Ser Leu Val Lys Ile Lys Phe Arg Glu Glu Pro
 85 90 95

Gly Cys Cys Ile Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro
 100 105 110

Val Leu Val Ala Leu Ala Leu Ile Glu Gly Gly Met Lys Tyr Glu Asp
 115 120 125

Ala Val Gln Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys
 130 135 140

Gln Leu Leu Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe
 145 150 155 160

Lys Asp Ser Asn Gly His Arg Asn Asn Cys Cys Ile Gln
 165 170

<E10> 34
 <E11> 167
 <E12> PRT
 <E13> homo sapiens

<400> 34

Met Asn Arg Pro Ala Pro Val Glu Ile Ser Tyr Glu Asn Met Arg Phe
 1 5 10 15

Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys Phe Thr Glu
 20 25 30

Glu Leu Lys Lys Tyr Gly Val Thr Thr Leu Val Arg Val Cys Asp Ala
 35 40 45

Thr Tyr Asp Lys Ala Pro Val Glu Lys Glu Gly Ile His Val Leu Asp
 50 55 60

Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Asn Gln Ile Val Asp Asp
 65 70 75 80

Trp Leu Asn Leu Leu Lys Thr Lys Phe Arg Glu Glu Pro Gly Cys Cys
 85 90 95

Val Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro Val Leu Val
 100 105 110

Ala Leu Ala Leu Ile Glu Cys Gly Met Lys Tyr Glu Asp Ala Val Gln
 115 120 125

Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys Gln Leu Leu
 130 135 140

Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe Arg Asp Thr
 145 150 155 160

Asn Gly His Cys Cys Val Gln
 165

<E10> 35
 <E11> 167
 <E12> PRT
 <E13> Mus musculus

<400> 35

Met Asn Arg Pro Ala Pro Val Glu Ile Ser Tyr Glu Asn Met Arg Phe
 1 5 10 15

Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys Phe Thr Glu
 20 25 30
 Glu Leu Lys Lys Tyr Gly Val Thr Thr Leu Val Arg Val Cys Asp Ala
 35 40 45
 Thr Tyr Asp Lys Ala Pro Val Glu Lys Glu Gly Ile His Val Leu Asp
 50 55 60
 Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Asn Gln Ile Val Asp Asp
 65 70 75 80
 Trp Leu Asn Leu Leu Lys Thr Leu Phe Arg Glu Glu Pro Gly Cys Cys
 85 90 95
 Val Ala Val His Cys Val Ala Gly Ile Gly Arg Ala Pro Val Leu Val
 100 105 110
 Ala Leu Ala Leu Ile Glu Cys Gly Met Lys Tyr Glu Asp Ala Val Gln
 115 120 125
 Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys Gln Leu Leu
 130 135 140
 Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe Arg Asp Thr
 145 150 155 160
 Asn Gly His Cys Cys Val Gln
 165

<210> 36
 <211> 178
 <212> PRT
 <213> Drosophila melanogaster

<400> 36

Met Ser Ile Thr Met Arg Gln Lys Asp Leu Arg Pro Ala Pro Ala Leu
 1 5 10 15
 Ile Glu Tyr Lys Gly Met Lys Phe Leu Ile Thr Asp Arg Pro Ser Asp
 20 25 30
 Ile Thr Ile Asn His Tyr Ile Met Glu Leu Lys Lys Asn Asn Val Asn
 35 40 45
 Thr Val Val Arg Val Cys Glu Pro Ser Tyr Asn Thr Asp Glu Leu Glu
 50 55 60
 Thr Gln Gly Ile Thr Val Lys Asp Leu Ala Phe Glu Asp Gly Thr Phe
 65 70 75 80
 Pro Pro Gln Gln Val Val Asp Glu Trp Phe Glu Phe Phe Val Val Leu
 85 90 95
 Tyr Arg Tyr Gln Gln Asn Pro Glu Ala Cys Val Ala Val His Cys Val
 100 105 110

Ala Gly Leu Gly Arg Ala Pro Val Leu Val Ala Leu Ala Leu Ile Glu
115 120 125

Leu Gly Leu Lys Tyr Glu Ala Ala Val Glu Met Ile Arg Asp Lys Arg
130 135 140

Arg Gly Ala Ile Asn Ala Lys Gln Leu Ser Phe Leu Glu Lys Tyr Lys
145 150 155 160

Pro Lys Ala Arg Leu Lys His Lys Asn Gly His Lys Asn Ser Cys Ser
165 170 175

Val Gln

<210> 37

<211> 1705

<212> PRT

<213> Mus musculus

<400> 37

Met Arg Pro Leu Ile Leu Leu Ala Ala Leu Leu Trp Leu Gln Asp Ser
1 5 10 15

Leu Ala Gln Glu Asp Val Cys Ser Ser Leu Asp Gly Ser Pro Asp Arg
20 25 30

Gln Gly Gly Gly Pro Pro Leu Ser Val Asn Val Ser Ser Arg Gly Lys
35 40 45

Pro Thr Ser Leu Phe Leu Ser Trp Val Ala Ala Glu Pro Gly Gly Phe
50 55 60

Asp Tyr Ala Leu Cys Leu Arg Ala Met Asn Leu Ser Gly Phe Pro Glu
65 70 75 80

Gly Gln Gln Leu Gln Ala His Thr Asn Glu Ser Ser Phe Glu Phe His
85 90 95

Gly Leu Val Pro Gly Ser Arg Tyr Gln Leu Glu Leu Thr Val Leu Arg
100 105 110

Pro Cys Trp Gln Asn Val Thr Ile Thr Leu Thr Ala Arg Thr Ala Pro
115 120 125

Thr Val Val Arg Gly Leu Gln Leu His Ser Thr Gly Ser Pro Ala Ser
130 135 140

Leu Glu Ala Ser Trp Ser Asp Ala Ser Gly Asp Gln Asp Ser Tyr Gln
145 150 155 160

Leu Leu Leu Tyr His Pro Glu Ser His Thr Leu Ala Cys Asn Val Ser
165 170 175

Val Ser Pro Asp Thr Leu Ser Tyr Asn Phe Gly Asp Leu Leu Pro Gly

180					185					190					
Ser	Gln	Tyr	Val	Leu	Glu	Val	Ile	Thr	Trp	Ala	Gly	Ser	Leu	His	Ala
195					200					205					
Lys	Thr	Ser	Ile	Leu	Gln	Trp	Thr	Glu	Pro	Val	Pro	Pro	Asp	His	Leu
210					215					220					
Thr	Leu	Arg	Ala	Leu	Gly	Thr	Ser	Ser	Leu	Gln	Ala	Phe	Trp	Asn	Ser
225					230					235					
Ser	Glu	Gly	Ala	Thr	Trp	Phe	His	Leu	Ile	Leu	Thr	Asp	Leu	Leu	Glu
245					250					255					
Gly	Thr	Asn	Leu	Thr	Lys	Val	Val	Arg	Gln	Gly	Ile	Ser	Thr	His	Thr
260					265					270					
Phe	Leu	Arg	Leu	Ser	Pro	Gly	Thr	Pro	Tyr	Gln	Leu	Lys	Ile	Cys	Ala
275					280					285					
Ala	Ala	Gly	Pro	His	Gln	Ile	Trp	Gly	Pro	Asn	Ala	Thr	Glu	Trp	Thr
290					295					300					
Tyr	Pro	Ser	Tyr	Pro	Ser	Asp	Leu	Val	Leu	Thr	Pro	Leu	Trp	Asn	Glu
305					310					315					
Leu	Trp	Ala	Ser	Trp	Lys	Ala	Gly	Gln	Gly	Ala	Arg	Asp	Gly	Tyr	Val
325					330					335					
Leu	Lys	Leu	Ser	Gly	Pro	Val	Glu	Asn	Thr	Thr	Thr	Leu	Gly	Pro	Glu
340					345					350					
Glu	Cys	Asn	Ala	Val	Phe	Pro	Gly	Pro	Leu	Pro	Pro	Gly	His	Tyr	Thr
355					360					365					
Leu	Gly	Leu	Arg	Val	Leu	Ala	Gly	Pro	Tyr	Asp	Ala	Trp	Val	Glu	Gly
370					375					380					
Ser	Ile	Trp	Leu	Ala	Glu	Ser	Ala	Ala	Arg	Pro	Met	Glu	Val	Pro	Gly
385					390					395					
Ala	Arg	Leu	Trp	Leu	Glu	Gly	Leu	Glu	Ala	Thr	Lys	Gln	Pro	Gly	Arg
405					410					415					
Arg	Ala	Leu	Leu	Tyr	Ser	Val	Asp	Ala	Pro	Gly	Leu	Leu	Gly	Asn	Ile
420					425					430					
Ser	Val	Ser	Ser	Gly	Ala	Thr	His	Val	Thr	Phe	Cys	Gly	Leu	Val	Pro
435					440					445					
Gly	Ala	His	Tyr	Arg	Val	Asp	Ile	Ala	Ser	Ser	Met	Gly	Asp	Ile	Thr
450					455					460					
Gln	Ser	Leu	Thr	Gly	Tyr	Thr	Ser	Pro	Leu	Pro	Pro	Gln	Ser	Leu	Glu
465					470					475					
Ile	Ile	Ser	Arg	Asn	Ser	Pro	Ser	Asp	Leu	Thr	Ile	Gly	Trp	Ala	Pro

485					490					495						
Ala	Pro	Gly	Gln	Met	Glu	Gly	Tyr	Lys	Val	Thr	Trp	His	Gln	Asp	Gly	
500					505					510						
Ser	Gln	Arg	Ser	Pro	Gly	Asp	Leu	Val	Asp	Leu	Gly	Pro	Asp	Ile	Ser	
515					520					525						
Ser	Leu	Thr	Leu	Lys	Ser	Leu	Val	Pro	Gly	Ser	Cys	Tyr	Thr	Val	Ser	
530					535					540						
Ala	Trp	Ala	Trp	Ser	Gly	Asn	Leu	Ser	Ser	Asp	Ser	Gln	Lys	Ile	His	
545					550					555					560	
Ser	Cys	Thr	Arg	Pro	Ala	Pro	Pro	Thr	Asn	Leu	Ser	Leu	Gly	Phe	Ala	
565					570					575						
His	Gln	Pro	Ala	Thr	Leu	Arg	Ala	Ser	Trp	Cys	His	Pro	Pro	Gly	Gly	
580					585					590						
Arg	Asp	Ala	Phe	Gln	Leu	Arg	Leu	Tyr	Arg	Leu	Arg	Pro	Leu	Thr	Leu	
595					600					605						
Glu	Ser	Glu	Lys	Ile	Leu	Ser	Gln	Glu	Ala	Gln	Asn	Phe	Ser	Trp	Ala	
610					615					620						
Gln	Leu	Pro	Ala	Gly	Tyr	Glu	Phe	Gln	Val	Gln	Leu	Ser	Thr	Leu	Trp	
625					630					635					640	
Gly	Ser	Glu	Glu	Ser	Gly	Ser	Ala	Asn	Thr	Thr	Gly	Trp	Thr	Pro	Pro	
645					650					655						
Ser	Ala	Pro	Thr	Leu	Val	Asn	Val	Thr	Ser	Glu	Ala	Pro	Thr	Gln	Leu	
660					665					670						
His	Val	Ser	Trp	Val	His	Ala	Ala	Gly	Asp	Arg	Ser	Ser	Tyr	Gln	Val	
675					680					685						
Thr	Leu	Tyr	Gln	Glu	Ser	Thr	Arg	Thr	Ala	Thr	Ser	Ile	Val	Gly	Pro	
690					695					700						
Lys	Ala	Asp	Ser	Thr	Ser	Phe	Trp	Gly	Leu	Thr	Pro	Gly	Thr	Lys	Tyr	
705					710					715					720	
Lys	Val	Glu	Ala	Ile	Ser	Trp	Ala	Gly	Pro	Leu	Tyr	Thr	Ala	Ala	Ala	
725					730					735						
Asn	Val	Ser	Ala	Trp	Thr	Tyr	Pro	Leu	Thr	Pro	Asn	Glu	Leu	Leu	Ala	
740					745					750						
Ser	Met	Gln	Ala	Gly	Ser	Ala	Val	Val	Asn	Leu	Ala	Trp	Pro	Ser	Gly	
755					760					765						
Pro	Leu	Gly	Gln	Gly	Thr	Cys	His	Ala	Gln	Leu	Ser	Asp	Ala	Gly	His	
770					775					780						
Leu	Ser	Trp	Glu	Gln	Pro	Leu	Ser	Leu	Gly	Gln	Asp	Leu	Leu	Met	Leu	

785		790		795		800
Arg Asn Leu Ile Pro Gly His Thr Val Ser Leu Ser Val Lys Cys Arg						
	805			810		815
Ala Gly Pro Leu Gln Ala Ser Thr His Pro Leu Val Leu Ser Val Glu						
	820			825		830
Pro Gly Pro Val Glu Asp Val Phe Cys Gln Pro Glu Ala Thr Tyr Leu						
	835			840		845
Ser Leu Asn Trp Thr Met Pro Thr Gly Asp Val Ala Val Cys Leu Val						
	850			855		860
Glu Val Glu Gln Leu Val Pro Gly Gly Ser Ala His Phe Val Phe Gln						
	865			870		875
Val Asn Thr Ser Glu Asp Ala Leu Leu Leu Pro Asn Leu Thr Pro Thr						
	885			890		895
Thr Ser Tyr Arg Leu Ser Leu Thr Val Leu Gly Gly Asn Arg Gln Trp						
	900			905		910
Ser Arg Ala Val Thr Leu Val Cys Thr Thr Ser Ala Glu Val Trp His						
	915			920		925
Pro Pro Glu Leu Ala Glu Ala Pro Gln Val Glu Leu Gly Thr Gly Met						
	930			935		940
Gly Val Thr Val Thr Arg Gly Met Phe Gly Lys Asp Asp Gly Gln Ile						
	945			950		955
Gln Trp Tyr Gly Ile Ile Ala Thr Ile Asn Met Thr Leu Ala Gln Pro						
	965			970		975
Ser Gln Glu Ala Ile Asn His Thr Trp Tyr Asp His Tyr Tyr Arg Gly						
	980			985		990
His Asp Ser Tyr Leu Ala Leu Leu Phe Pro Asn Pro Phe Tyr Pro Glu						
	995			1000		1005
Pro Trp Ala Val Pro Arg Ser Trp Thr Val Pro Val Gly Thr Glu						
	1010			1015		1020
Asp Cys Asp Asn Thr Gln Glu Ile Cys Asn Gly His Leu Lys Pro						
	1025			1030		1035
Gly Phe Gln Tyr Arg Phe Ser Ile Ala Ala Phe Ser Arg Leu Ser						
	1040			1045		1050
Ser Pro Glu Thr Ile Leu Ala Phe Ser Ala Phe Ser Glu Pro Gln						
	1055			1060		1065
Ala Ser Ile Ser Leu Val Ala Met Pro Leu Thr Val Met Met Gly						
	1070			1075		1080
Thr Val Val Gly Cys Ile Ile Ile Val Cys Ala Val Leu Cys Leu						

1085		1090		1095
Leu Cys Arg Arg Arg Leu	Lys Gly Pro Arg Ser	Glu Lys Asn Gly		
1100	1105	1110		
Phe Ser Gln Glu Leu Met	Pro Tyr Asn Leu Trp	Arg Thr His Arg		
1115	1120	1125		
Pro Ile Pro Ser His Ser	Phe Arg Gln Ser Tyr	Glu Ala Lys Ser		
1130	1135	1140		
Ala Arg Ala His Gln Ala	Phe Phe Gln Glu Phe	Glu Glu Leu Lys		
1145	1150	1155		
Glu Val Gly Lys Asp Gln	Pro Arg Leu Glu Ala	Gln His Pro Ala		
1160	1165	1170		
Asn Ile Thr Lys Asn Arg	Tyr Pro His Val Leu	Pro Tyr Asp His		
1175	1180	1185		
Ser Arg Val Arg Leu Thr	Gln Leu Ser Gly Glu	Pro His Ser Asp		
1190	1195	1200		
Tyr Ile Asn Ala Asn Phe	Ile Pro Gly Tyr Ser	His Pro Gln Glu		
1205	1210	1215		
Ile Ile Ala Thr Gln Gly	Pro Leu Lys Lys Thr	Val Glu Asp Phe		
1220	1225	1230		
Trp Arg Leu Val Trp Glu	Gln Gln Val His Val	Ile Ile Met Leu		
1235	1240	1245		
Thr Val Gly Met Glu Asn	Gly Arg Val Leu Cys	Glu His Tyr Trp		
1250	1255	1260		
Pro Val Asn Ser Thr Pro	Val Thr His Gly His	Ile Thr Thr His		
1265	1270	1275		
Leu Leu Ala Glu Glu Ser	Glu Asp Glu Trp Thr	Arg Arg Glu Phe		
1280	1285	1290		
Gln Leu Gln His Gly Ala	Glu Gln Lys Gln Arg	Arg Val Lys Gln		
1295	1300	1305		
Leu Gln Phe Thr Thr Trp	Pro Asp His Ser Val	Pro Glu Ala Pro		
1310	1315	1320		
Ser Ser Leu Leu Ala Phe	Val Glu Leu Val Gln	Glu Glu Val Lys		
1325	1330	1335		
Ala Thr Gln Gly Lys Gly	Pro Ile Leu Val His	Cys Ser Ala Gly		
1340	1345	1350		
Val Gly Arg Thr Gly Thr	Phe Val Ala Leu Leu	Pro Ala Val Arg		
1355	1360	1365		
Gln Leu Glu Glu Glu Gln	Val Val Asp Val Phe	Asn Thr Val Tyr		

1370	1375	1380
Ile Leu Arg Leu His Arg Pro Leu Met Ile Gln Thr Leu Ser Gln		
1385	1390	1395
Tyr Ile Phe Leu His Ser Cys Leu Leu Asn Lys Ile Leu Glu Gly		
1400	1405	1410
Pro Ser Asp Ala Ser Asp Ser Gly Pro Ile Pro Val Met Asn Phe		
1415	1420	1425
Ala Gln Ala Cys Ala Lys Arg Ala Ala Asn Ala Asn Ala Gly Phe		
1430	1435	1440
Leu Lys Glu Tyr Arg Leu Leu Lys Gln Ala Ile Lys Asp Glu Thr		
1445	1450	1455
Gly Ser Leu Leu Pro Ser Pro Asp Tyr Asn Gln Asn Ser Ile Ala		
1460	1465	1470
Ser Cys His His Ser Gln Glu Gln Leu Ala Leu Val Glu Glu Ser		
1475	1480	1485
Pro Ala Asp Asn Met Leu Ala Ala Ser Leu Phe Pro Gly Gly Pro		
1490	1495	1500
Ser Gly Arg Asp His Val Val Leu Thr Gly Ser Ala Gly Pro Lys		
1505	1510	1515
Glu Leu Trp Glu Met Val Trp Glu His Gly Ala Tyr Val Leu Val		
1520	1525	1530
Ser Leu Gly Leu Pro Asp Thr Lys Glu Lys Pro Gln Asp Ile Trp		
1535	1540	1545
Pro Met Glu Met Gln Pro Ile Val Thr Asp Met Val Thr Val His		
1550	1555	1560
Arg Val Ala Glu Ser Asn Thr Ala Gly Trp Pro Ser Thr Leu Ile		
1565	1570	1575
Arg Val Ile His Gly Asp Ser Gly Thr Glu Arg Gln Val Gln Cys		
1580	1585	1590
Leu Gln Phe Pro His Cys Glu Thr Gly Ser Glu Leu Pro Ala Asn		
1595	1600	1605
Thr Leu Leu Thr Phe Leu Asp Ala Val Gly Gln Cys Cys Ser Arg		
1610	1615	1620
Gly Asn Ser Lys Lys Pro Gly Thr Leu Leu Ser His Ser Ser Lys		
1625	1630	1635
Val Thr Asn Gln Leu Ser Thr Phe Leu Ala Met Glu Gln Leu Leu		
1640	1645	1650
Gln Gln Ala Gly Thr Glu Arg Thr Val Asp Val Phe Ser Val Ala		

1555	1560	1565
Leu Lys Gln Thr Gln Ala Cys Gly Leu Lys Thr Pro Thr Leu Glu		
1570	1575	1580
Gln Tyr Ile Tyr Leu Tyr Asn Cys Leu Asn Ser Ala Leu Arg Asn		
1585	1590	1595
Arg Leu Pro Arg Ala Arg Lys		
1700	1705	

<210> 38
 <211> 1711
 <212> PRT
 <213> Rattus norvegicus

<400> 38

Met Arg Pro Leu Ile Leu Leu Ala Ala Leu Leu Trp Leu Gln Gly Phe	
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Leu Ala Glu Asp Asp Ala Cys Ser Ser Leu Gly Gly Ser Pro Asp Arg	
20 25 30	
Gln Gly Gly Gly Pro Leu Leu Ser Val Asn Val Ser Ser His Gly Lys	
35 40 45	
Ser Thr Ser Leu Phe Leu Ser Trp Val Ala Ala Glu Leu Gly Gly Phe	
50 55 60	
Asp Tyr Ala Leu Ser Leu Arg Ser Val Asp Ser Ser Gly Ser Pro Glu	
65 70 75 80	
Gly Gln Gln Leu Gln Ala His Thr Asn Glu Ser Gly Phe Glu Phe His	
85 90 95	
Gly Leu Val Pro Gly Ser Arg Tyr Gln Leu Lys Leu Thr Val Leu Arg	
100 105 110	
Pro Cys Trp Gln Asn Val Thr Ile Thr Leu Thr Ala Arg Thr Ala Pro	
115 120 125	
Thr Val Val Arg Gly Leu Gln Leu His Ser Ala Gly Ser Pro Ala Arg	
130 135 140	
Leu Glu Ala Ser Trp Ser Asp Ala Pro Gly Asp Gln Asp Ser Tyr Gln	
145 150 155 160	
Leu Leu Leu Tyr His Leu Glu Ser Gln Thr Leu Ala Cys Asn Val Ser	
165 170 175	
Val Ser Pro Asp Thr Leu Ser Tyr Ser Phe Gly Asp Leu Leu Pro Gly	
180 185 190	
Thr Gln Tyr Val Leu Glu Val Ile Thr Trp Ala Gly Ser Leu His Ala	
195 200 205	

Lys Thr Ser Ile Leu Gln Trp Thr Glu Pro Val Pro Pro Asp His Leu
 210 215 220
 Ala Leu Arg Ala Leu Gly Thr Ser Ser Leu Gln Ala Phe Trp Asn Ser
 225 230 235 240
 Ser Glu Gly Ala Thr Ser Phe His Leu Met Leu Thr Asp Leu Leu Gly
 245 250 255
 Gly Thr Asn Thr Thr Ala Val Ile Arg Gln Gly Val Ser Thr His Thr
 260 265 270
 Phe Leu His Leu Ser Pro Gly Thr Pro His Glu Leu Lys Ile Cys Ala
 275 280 285
 Ser Ala Gly Pro His Gln Ile Trp Gly Pro Ser Ala Thr Glu Trp Thr
 290 295 300
 Tyr Pro Ser Tyr Pro Ser Asp Leu Val Leu Thr Pro Leu Arg Asn Glu
 305 310 315 320
 Leu Trp Ala Ser Trp Lys Ala Gly Leu Gly Ala Arg Asp Gly Tyr Val
 325 330 335
 Leu Lys Leu Ser Gly Pro Met Glu Ser Thr Ser Thr Leu Gly Pro Glu
 340 345 350
 Glu Cys Asn Ala Val Phe Pro Gly Pro Leu Pro Pro Gly His Tyr Thr
 355 360 365
 Leu Gln Leu Lys Val Leu Ala Gly Pro Tyr Asp Ala Trp Val Glu Gly
 370 375 380
 Ser Thr Trp Leu Ala Glu Ser Ala Ala Leu Pro Arg Glu Val Pro Gly
 385 390 395 400
 Ala Arg Leu Trp Leu Asp Gly Leu Glu Ala Ser Lys Gln Pro Gly Arg
 405 410 415
 Arg Ala Leu Leu Tyr Ser Asp Asp Ala Pro Gly Ser Leu Gly Asn Ile
 420 425 430
 Ser Val Pro Ser Gly Ala Thr His Val Ile Phe Cys Gly Leu Val Pro
 435 440 445
 Gly Ala His Tyr Arg Val Asp Ile Ala Ser Ser Thr Gly Asp Ile Ser
 450 455 460
 Gln Ser Ile Ser Gly Tyr Thr Ser Pro Leu Pro Pro Gln Ser Leu Glu
 465 470 475 480
 Val Ile Ser Arg Ser Ser Pro Ser Asp Leu Thr Ile Ala Trp Gly Pro
 485 490 495
 Ala Pro Gly Gln Leu Glu Gly Tyr Lys Val Thr Trp His Gln Asp Gly
 500 505 510

Ser Gln Arg Ser Pro Gly Asp Leu Val Asp Leu Gly Pro Asp Thr Leu
 515 520 525
 Ser Leu Thr Leu Lys Ser Leu Val Pro Gly Ser Ser Tyr Thr Val Ser
 530 535 540
 Ala Trp Ala Trp Ala Gly Asn Leu Gly Ser Asp Ser Gln Lys Ile His
 545 550 555 560
 Ser Cys Thr Arg Pro Ala Pro Pro Thr Asn Leu Ser Leu Gly Phe Ala
 565 570 575
 His Gln Pro Ala Ala Leu Lys Ala Ser Trp Tyr His Pro Pro Gly Gly
 580 585 590
 Arg Asp Ala Phe His Leu Arg Leu Tyr Arg Leu Arg Pro Leu Thr Leu
 595 600 605
 Glu Ser Glu Lys Val Leu Pro Arg Glu Ala Gln Asn Phe Ser Trp Ala
 610 615 620
 Gln Leu Thr Ala Gly Cys Glu Phe Gln Val Gln Leu Ser Thr Leu Trp
 625 630 635 640
 Gly Ser Glu Arg Ser Ser Ser Ala Asn Ala Thr Gly Trp Thr Pro Pro
 645 650 655
 Ser Ala Pro Thr Leu Val Asn Val Thr Ser Asp Ala Pro Thr Gln Leu
 660 665 670
 Gln Val Ser Trp Ala His Val Pro Gly Gly Arg Ser Arg Tyr Gln Val
 675 680 685
 Thr Leu Tyr Gln Glu Ser Thr Arg Thr Ala Thr Ser Ile Met Gly Pro
 690 695 700
 Lys Glu Asp Gly Thr Ser Phe Leu Gly Leu Thr Pro Gly Thr Lys Tyr
 705 710 715 720
 Lys Val Glu Val Ile Ser Trp Ala Gly Pro Leu Tyr Thr Ala Ala Ala
 725 730 735
 Asn Val Ser Ala Trp Thr Tyr Pro Leu Ile Pro Asn Glu Leu Leu Val
 740 745 750
 Ser Met Gln Ala Gly Ser Ala Val Val Asn Leu Ala Trp Pro Ser Gly
 755 760 765
 Pro Leu Gly Gln Gly Ala Cys His Ala Gln Leu Ser Asp Ala Gly His
 770 775 780
 Leu Ser Trp Glu Gln Pro Leu Lys Leu Gly Gln Glu Leu Phe Met Leu
 785 790 795 800
 Arg Asp Leu Thr Pro Gly His Thr Ile Ser Met Ser Val Arg Cys Arg
 805 810 815

Ala Gly Pro Leu Gln Ala Ser Thr His Leu Val Val Leu Ser Val Glu
 820 825 830
 Pro Gly Pro Val Glu Asp Val Leu Cys His Pro Glu Ala Thr Tyr Leu
 835 840 845
 Ala Leu Asn Trp Thr Met Pro Ala Gly Asp Val Asp Val Cys Leu Val
 850 855 860
 Val Val Glu Arg Leu Val Pro Gly Gly Gly Thr His Phe Val Phe Gln
 865 870 875 880
 Val Asn Thr Ser Gly Asp Ala Leu Leu Leu Pro Asn Leu Met Pro Thr
 885 890 895
 Thr Ser Tyr Arg Leu Ser Leu Thr Val Leu Gly Arg Asn Ser Arg Trp
 900 905 910
 Ser Arg Ala Val Ser Leu Val Cys Ser Thr Ser Ala Glu Ala Trp His
 915 920 925
 Pro Pro Glu Leu Ala Glu Pro Pro Gln Val Glu Leu Gly Thr Gly Met
 930 935 940
 Gly Val Thr Val Met Arg Gly Met Phe Gly Lys Asp Asp Gly Gln Ile
 945 950 955 960
 Gln Trp Tyr Gly Ile Ile Ala Thr Ile Asn Met Thr Leu Ala Gln Pro
 965 970 975
 Ser Arg Glu Ala Ile Asn Tyr Thr Trp Tyr Asp His Tyr Tyr Arg Gly
 980 985 990
 Cys Glu Ser Phe Leu Ala Leu Leu Phe Pro Asn Pro Phe Tyr Pro Glu
 995 1000 1005
 Pro Trp Ala Gly Pro Arg Ser Trp Thr Val Pro Val Gly Thr Glu
 1010 1015 1020
 Asp Cys Asp Asn Thr Gln Glu Ile Cys Asn Gly Arg Leu Lys Ser
 1025 1030 1035
 Gly Phe Gln Tyr Arg Phe Ser Val Val Ala Phe Ser Arg Leu Asn
 1040 1045 1050
 Thr Pro Glu Thr Ile Leu Ala Phe Ser Ala Phe Ser Glu Pro Arg
 1055 1060 1065
 Ala Ser Ile Ser Leu Ala Ile Ile Pro Leu Thr Val Met Leu Gly
 1070 1075 1080
 Ala Val Val Gly Ser Ile Val Ile Val Cys Ala Val Leu Cys Leu
 1085 1090 1095
 Leu Arg Trp Arg Cys Leu Lys Gly Pro Arg Ser Glu Lys Asp Gly
 1100 1105 1110

Phe	Ser	Lys	Glu	Leu	Met	Pro	Tyr	Asn	Leu	Trp	Arg	Thr	His	Arg	
1115						1130					1135				
Pro	Ile	Pro	Ile	His	Ser	Phe	Arg	Gln	Ser	Tyr	Glu	Ala	Lys	Ser	
1130						1135					1140				
Ala	His	Ala	His	Gln	Thr	Phe	Phe	Gln	Glu	Phe	Glu	Glu	Leu	Lys	
1145						1150					1155				
Glu	Val	Gly	Lys	Asp	Gln	Pro	Arg	Leu	Glu	Ala	Glu	His	Pro	Asp	
1150						1155					1170				
Asn	Ile	Ile	Lys	Asn	Arg	Tyr	Pro	His	Val	Leu	Pro	Tyr	Asp	His	
1175						1180					1185				
Ser	Arg	Val	Arg	Leu	Thr	Gln	Leu	Pro	Gly	Glu	Pro	His	Ser	Asp	
1190						1195					1200				
Tyr	Ile	Asn	Ala	Asn	Phe	Ile	Pro	Gly	Tyr	Ser	His	Thr	Gln	Glu	
1205						1210					1215				
Ile	Ile	Ala	Thr	Gln	Gly	Pro	Leu	Lys	Lys	Thr	Leu	Glu	Asp	Phe	
1220						1225					1230				
Trp	Arg	Leu	Val	Trp	Glu	Gln	Gln	Val	His	Val	Ile	Ile	Met	Leu	
1235						1240					1245				
Thr	Val	Gly	Met	Glu	Asn	Gly	Arg	Val	Leu	Cys	Glu	His	Tyr	Trp	
1250						1255					1260				
Pro	Ala	Asn	Ser	Thr	Pro	Val	Thr	His	Gly	His	Ile	Thr	Ile	His	
1265						1270					1275				
Leu	Leu	Ala	Glu	Glu	Pro	Glu	Asp	Glu	Trp	Thr	Arg	Arg	Glu	Phe	
1280						1285					1290				
Gln	Leu	Gln	His	Gly	Thr	Glu	Gln	Lys	Gln	Arg	Arg	Val	Lys	Gln	
1295						1300					1305				
Leu	Gln	Phe	Thr	Thr	Trp	Pro	Asp	His	Ser	Val	Pro	Glu	Ala	Pro	
1310						1315					1320				
Ser	Ser	Leu	Leu	Ala	Phe	Val	Glu	Leu	Val	Gln	Glu	Gln	Val	Gln	
1325						1330					1335				
Ala	Thr	Gln	Gly	Lys	Gly	Pro	Ile	Leu	Val	His	Cys	Ser	Ala	Gly	
1340						1345					1350				
Val	Gly	Arg	Thr	Gly	Thr	Phe	Val	Ala	Leu	Leu	Arg	Leu	Leu	Arg	
1355						1360					1365				
Gln	Leu	Glu	Glu	Glu	Lys	Val	Ala	Asp	Val	Phe	Asn	Thr	Val	Tyr	
1370						1375					1380				
Ile	Leu	Arg	Leu	His	Arg	Pro	Leu	Met	Ile	Gln	Thr	Leu	Ser	Gln	
1385						1390					1395				

Tyr	Ile	Phe	Leu	His	Ser	Cys	Leu	Leu	Asn	Lys	Ile	Leu	Glu	Gly
1400						1405					1410			
Pro	Pro	Asp	Ser	Ser	Asp	Ser	Gly	Pro	Ile	Ser	Val	Met	Asp	Phe
1415						1420					1425			
Ala	Gln	Ala	Cys	Ala	Lys	Arg	Ala	Ala	Asn	Ala	Asn	Ala	Gly	Phe
1430						1435					1440			
Leu	Lys	Glu	Tyr	Lys	Leu	Leu	Lys	Gln	Ala	Ile	Lys	Asp	Gly	Thr
1445						1450					1455			
Gly	Ser	Leu	Leu	Pro	Pro	Pro	Asp	Tyr	Asn	Gln	Asn	Ser	Ile	Val
1460						1465					1470			
Ser	Arg	Arg	His	Ser	Gln	Glu	Gln	Phe	Ala	Leu	Val	Glu	Glu	Cys
1475						1480					1485			
Pro	Gln	Asp	Ser	Met	Leu	Glu	Ala	Ser	Leu	Phe	Pro	Gly	Gly	Pro
1490						1495					1500			
Ser	Gly	Cys	Asp	His	Val	Val	Leu	Thr	Gly	Ser	Ala	Gly	Pro	Lys
1505						1510					1515			
Glu	Leu	Trp	Glu	Met	Val	Trp	Glu	His	Asp	Ala	His	Val	Leu	Val
1520						1525					1530			
Ser	Leu	Gly	Leu	Pro	Asp	Thr	Lys	Glu	Lys	Pro	Pro	Asp	Ile	Trp
1535						1540					1545			
Pro	Val	Glu	Met	Gln	Pro	Ile	Val	Thr	Asp	Met	Val	Thr	Val	His
1550						1555					1560			
Arg	Val	Ser	Glu	Ser	Asn	Thr	Thr	Thr	Gly	Trp	Pro	Ser	Thr	Leu
1565						1570					1575			
Phe	Arg	Val	Ile	His	Gly	Glu	Ser	Gly	Lys	Glu	Arg	Gln	Val	Gln
1580						1585					1590			
Cys	Leu	Gln	Phe	Pro	Cys	Ser	Glu	Ser	Gly	Cys	Glu	Leu	Pro	Ala
1595						1600					1605			
Asn	Thr	Leu	Leu	Thr	Phe	Leu	Asp	Ala	Val	Gly	Gln	Cys	Cys	Phe
1610						1615					1620			
Arg	Gly	Lys	Ser	Lys	Lys	Pro	Gly	Thr	Leu	Leu	Ser	His	Ser	Ser
1625						1630					1635			
Lys	Asn	Thr	Asn	Gln	Leu	Gly	Thr	Phe	Leu	Ala	Met	Glu	Gln	Leu
1640						1645					1650			
Leu	Gln	Gln	Ala	Gly	Thr	Glu	Arg	Thr	Val	Asp	Val	Phe	Asn	Val
1655						1660					1665			
Ala	Leu	Lys	Gln	Ser	Gln	Ala	Cys	Gly	Leu	Met	Thr	Pro	Thr	Leu
1670						1675					1680			

Glu Gln Tyr Ile Tyr Leu Tyr Asn Cys Leu Asn Ser Ala Leu Leu
 1685 1690 1695

Asn Gly Leu Pro Arg Ala Gly Lys Trp Pro Ala Pro Cys
 1700 1705 1710

<210> 39
 <211> 625
 <212> PRT
 <213> HOMO SAPIENS

<400> 39

Met Ala Gly Asp Arg Leu Pro Arg Lys Val Met Asp Ala Lys Lys Leu
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Ala Ser Leu Leu Arg Gly Gly Pro Gly Gly Pro Leu Val Ile Asp Ser
 20 25 30

Arg Ser Phe Val Glu Tyr Asn Ser Trp His Val Leu Ser Ser Val Asn
 35 40 45

Ile Cys Cys Ser Lys Leu Val Lys Arg Arg Leu Gln Gln Gly Lys Val
 50 55 60

Thr Ile Ala Glu Leu Ile Gln Pro Ala Ala Arg Ser Gln Val Glu Ala
 65 70 75 80

Thr Glu Pro Gln Asp Val Val Val Tyr Asp Gln Ser Thr Arg Asp Ala
 85 90 95

Ser Val Leu Ala Ala Asp Ser Phe Leu Ser Ile Leu Leu Ser Lys Leu
 100 105 110

Asp Gly Cys Phe Asp Ser Val Ala Ile Leu Thr Gly Gly Phe Ala Thr
 115 120 125

Phe Ser Ser Cys Phe Pro Gly Leu Cys Glu Gly Lys Pro Ala Ala Leu
 130 135 140

Leu Pro Met Ser Leu Ser Gln Pro Cys Leu Pro Val Pro Ser Val Gly
 145 150 155 160

Leu Thr Arg Ile Leu Pro His Leu Tyr Leu Gly Ser Gln Lys Asp Val
 165 170 175

Leu Asn Lys Asp Leu Met Thr Gln Asn Gly Ile Ser Tyr Val Leu Asn
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Ala Ser Asn Ser Cys Pro Lys Pro Asp Phe Ile Cys Glu Ser Arg Phe
 195 200 205

Met Arg Val Pro Ile Asn Asp Asn Tyr Cys Glu Lys Leu Leu Pro Trp
 210 215 220

Leu Asp Lys Ser Ile Glu Phe Ile Asp Lys Ala Lys Leu Ser Ser Cys
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Gln	Val	Ile	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	245	250	255
Ala	Ile	Ala	Tyr	Ile	Met	Lys	Thr	Met	Gly	Met	Ser	Ser	Asp	Asp	Ala	260	265	270
Tyr	Arg	Phe	Val	Lys	Asp	Arg	Arg	Pro	Ser	Ile	Ser	Pro	Asn	Phe	Asn	275	280	285
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Ala	Leu	Gln	Gly	Asp	Pro	Gly	Thr	Pro	Ser	Gly	Thr	Pro	Glu	Pro	Pro	305	310	315
Pro	Ser	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Pro	Arg	Leu	Pro	Pro	Pro	Thr	325	330	335
Ser	Glu	Ser	Ala	Ala	Thr	Gly	Asn	Ala	Ala	Ala	Arg	Glu	Gly	Gly	Leu	340	345	350
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Ala	Tyr	Ala	Pro	Ser	Arg	Arg	Pro	Asp	Gly	Pro	Gly	Pro	Pro	Asp	Pro	405	410	415
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Ala	Arg	Pro	Arg	Pro	Arg	Arg	Arg	Pro	Arg	Pro	Pro	Ala	Gly	Ser	Pro	450	455	460
Ala	Arg	Ser	Pro	Ala	His	Ser	Leu	Gly	Leu	Asn	Phe	Gly	Asp	Ala	Ala	465	470	475
Arg	Gln	Thr	Pro	Arg	His	Gly	Leu	Ser	Ala	Leu	Ser	Ala	Pro	Gly	Leu	485	490	495
Pro	Gly	Pro	Gly	Gln	Pro	Ala	Gly	Pro	Gly	Ala	Trp	Ala	Pro	Pro	Leu	500	505	510
Asp	Ser	Pro	Gly	Thr	Pro	Ser	Pro	Asp	Gly	Pro	Trp	Cys	Phe	Ser	Pro	515	520	525
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Thr Glu Pro Gln Asp Val Val Val Tyr Asp Gln Ser Thr Arg Asp Ala
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Asp Gly Cys Phe Asp Ser Val Ala Ile Leu Thr Gly Gly Phe Ala Thr
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Leu Thr Arg Ile Leu Pro His Leu Tyr Leu Gly Ser Gln Lys Asp Val

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Met Arg Ile Pro Ile Asn Asp Asn Tyr Cys Glu Lys Leu Leu Pro Trp	210		215		210
Leu Asp Lys Ser Ile Glu Phe Ile Asp Lys Ala Lys Leu Ser Ser Cys	225		230		235
Gln Val Ile Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile	245		250		255
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Tyr Arg Phe Val Lys Asp Arg Arg Pro Ser Ile Ser Pro Asn Phe Asn	275		280		285
Phe Leu Gly Gln Leu Leu Glu Tyr Glu Arg Ser Leu Lys Leu Leu Ala	290		295		300
Ala Leu Gln Thr Asp Gly Pro His Leu Gly Thr Pro Glu Pro Leu Met	305		310		315
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Asp Pro Gly Glu Ala Pro Lys Leu Cys Lys Leu Asp Ser Pro Ser Gly	420		425		430
Gly Thr Leu Gly Leu Pro Ser Pro Ser Pro Asp Ser Pro Asp Ser Val	435		440		445
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 tcccgccagc cggcccggga 79

 <210> 51
 <211> 20
 <212> DNA
 <213> HOMO SAPIENS

 <400> 52
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 <210> 53
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 <212> DNA
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 <400> 53
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 <210> 54

<211> 30
 <212> DNA
 <213> HOMO SAPIENS

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<210> 56
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<210> 57
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<210> 59
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<210> 50
 <211> 30
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 <210> 53
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 cagcccagac tggaggetga 30

 <210> 54
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 <400> 55
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<210> 65
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 ctactacaaa gaactgttaa 30

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 <210> 69
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<210> 72
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<400> 71
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<210> 73
 <211> 80
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<400> 73
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 cagaccagac tggaggctga 30

<210> 74
 <211> 80
 <212> DNA
 <213> HOMO SAPIENS

<400> 74
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 aaagcctggt ggcctatgagc 30

<210> 75
 <211> 8
 <212> PRT
 <213> bacteriophage T7

<400> 75

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 76
 <211> 733
 <212> DNA
 <213> homo sapiens

<400> 76
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 tctcccgga ccttgagggt acatgggtgg tgggtggact aagccacgaa gacctgagg 150
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 200
 aggagcagta caacagcagc tacctgtgtg ccagcgtctt caccgtctg caccaggact 250

ggctgaatgg caaggagtag aagtgcgaagg tctccaacaa agcctccca accccatcg 360
 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac acctgcccc 420
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
 atccaagoga catcgccgtg gagtgggaga gcaatgggca gccggagAAC aactacaaga 540
 ccagcctcc cgtgctggac tccgaaggct ccttcttct ctacagcaag ctcccggtgg 600
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcac gaggctctgc 660
 acaaccacta caccgagaag agcctctccc tgtctccggg taaatgagtg cgaaggccgc 720
 gactctagag gat 733

<210> 77
 <211> 7
 <212> PRT
 <213> HOMO SAPIENS

<400> 77

Asp Tyr Ile Asn Ala Ser Asn
 1 5

<210> 78
 <211> 6
 <212> PRT
 <213> HOMO SAPIENS

<220>
 <221> VARIANT
 <222> (2)..(2)
 <223> wherein 'Xaa' is any amino acid.

<220>
 <221> VARIANT
 <222> (3)..(3)
 <223> wherein 'Xaa' is any amino acid.

<400> 78

Cys Xaa Xaa Tyr Trp Pro
 1 5

<210> 79
 <211> 9
 <212> PRT
 <213> HOMO SAPIENS

<220>
 <221> Variant
 <222> (5)..(5)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (6)..(6)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (7)..(7)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (8)..(8)

<223> wherein 'Xaa' is any amino acid.

<400> 79

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1 5

<210> 80

<211> 8

<212> PBT

<213> HOMO SAPIENS

<400> 80

Asp Asn Tyr Ile Asn Ala Ser Asn
1 5

<210> 81

<211> 6

<212> PBT

<213> HOMO SAPIENS

<220>

<221> Variant

<222> (2)..(2)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (3)..(3)

<223> wherein 'Xaa' is any amino acid.

<400> 81

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1 5

<210> 82
 <211> 9
 <212> PRT
 <213> HOMO SAPIENS

<220>
 <221> Variant
 <222> (5)..(5)
 <223> wherein 'Xaa' is any amino acid.

<220>
 <221> Variant
 <222> (5)..(6)
 <223> wherein 'Xaa' is any amino acid.

<220>
 <221> Variant
 <222> (7)..(7)
 <223> wherein 'Xaa' is any amino acid.

<220>
 <221> Variant
 <222> (8)..(8)
 <223> wherein 'Xaa' is any amino acid.

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 1 5

<210> 83
 <211> 511
 <212> DNA
 <213> homo sapiens

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 ggagttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180
 ggaagcatcc aggttccgga ctggcctttt gatgatggta cagcaccatc cagccagata 240
 attgataact ggttaaaact tatgaaaaat aaatttcatg aagatcctgg ttgttgattt 300
 gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgccc tagctttaat 360
 tgaagggtgga atgaaatatg aaaatgtagt acagttcatc agataaaagt gacatggaac 420
 ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gcttgcacct 480

cagaaatccc agaaataact gtttctttca g

511

<210> 84
<211> 157
<212> PRT
<213> homo sapiens

<400> 84

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20 25 30
Phe Leu Gln Glu Leu Lys Gln Asp Gly Val Thr Thr Ile Val Arg Val
35 40 45
Lys Ala Thr Tyr Asn Ile Ala Leu Leu Glu Lys Gly Ser Ile Gln Val
50 55 60
Pro Asp Trp Pro Phe Asp Asp Gly Thr Ala Pro Ser Ser Gln Ile Ile
65 70 75 80
Asp Asn Trp Leu Lys Leu Met Lys Asn Lys Phe His Glu Asp Pro Gly
85 90 95
Cys Cys Ile Ala Ile His Cys Val Val Gly Phe Gly Glu Leu Gln Leu
100 105 110
Leu Val Ala Leu Ala Leu Ile Glu Gly Gly Met Lys Tyr Glu Asn Val
115 120 125
Val Gln Phe Ile Arg Lys His Gly Thr Phe Asn Ser Lys Gln Leu Leu
130 135 140
Tyr Leu Glu Lys Tyr Cys Leu Lys Ile Cys Leu His Leu Arg Asn Pro
145 150 155 160
Arg Asn Asn Cys Phe Leu Gln
165

<210> 85
<211> 14
<212> PRT
<213> homo sapiens

<400> 85

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile
1 5 10

<210> 86
<211> 14
<212> PRT
<213> homo sapiens

<400> 85

Glu Ala Ile Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg
1 5 10

<210> 37

<211> 14

<212> PRT

<213> homo sapiens

<400> A7

Ile Gly Tyr Val Leu Asn Ala Ser Asn Thr Cys Pro Lys Pro
1 5 10

<210> 44

<211> 14

<212> PRT

<213> homo sapiens

<400> 66

Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu
1 5 10

<210> 89

<211> 14

<212> PRT

<213> homo sapiens

<400> 87

Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys
1 5 10

<210> 98

<211> 14

<212> PRT

<213> homo sapiens

<400> 98

Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu Leu Gly Lys
1 5 10

<210> 91

<211> 13

<212> PRT

<213> homo sapiens

<400> 91

Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala Leu Leu
1 5 10

<210> 92

<211> 12
<212> PPT
<213> homo sapiens

<400> 91

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1 5 10

<210> 91
<211> 13
<212> PPT
<213> homo sapiens

<400> 91

Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile
1 5 10

<210> 94
<211> 13
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<213> homo sapiens

<400> 94

Val Asp Ile Asp Cys Ser Gln Lys Val Val Val Tyr Asp
1 5 10

<210> 95
<211> 13
<212> PPT
<213> homo sapiens

<400> 95

Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe
1 5 10

<210> 96
<211> 13
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<400> 96

Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser
1 5 10

<210> 97
<211> 13
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<400> 97

Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln

1	5	10
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<210> 98
 <211> 13
 <212> PFT
 <213> homo sapiens

 <400> 98

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<210> 99
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 <212> PFT
 <213> homo sapiens

 <400> 99

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1			5						10			

<210> 100
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 <400> 100

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<210> 101
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 <212> PFT
 <213> homo sapiens

 <400> 101

Arg	Arg	Gln	Lys	Pro	Ser	Asp	Arg	Ala	Asp	Ser	Arg	Arg
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<210> 102
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 <212> PFT
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 <400> 102

Ser	Asp	Arg	Ala	Asp	Ser	Arg	Arg	Ser	Trp	His	Glu	Glu
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 <211> 23
 <212> PFT
 <213> homo sapiens

<400> 103

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Thr Ile Ala Ile Ala Tyr Ile
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<210> 104

<211> 39

<212> DNA

<213> Homo sapiens

<400> 104

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<210> 105

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<213> Homo sapiens

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<210> 106

<211> 39

<212> DNA

<213> Homo sapiens

<400> 106

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<210> 107

<211> 37

<212> DNA

<213> Homo sapiens

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<210> 108

<211> 5450

<212> DNA

<213> Homo sapiens

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<221> CDS

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<400> 108

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gtgacaactt tegtttccct ctgaggggaat tgggagggtcg ggggccccaa aagcttttcag	180
tccagtgtaa agctgttggg gggggggagc aaaggtaaag aatgatgtaa tgcgctggct	240
gctccaaagc atcttttgggt gtggaatggg tattccagtc atctctttat gaatcaaatg	300
tgaggggctg ctttgtggac ggagtccttt gcaagagcac atcaacggga aagagaaaga	360
gacattcact tggagggctc ttgtgaaaa tgggtttaac tctcttttg ccagtcacca	420
ccagcctgac ctcatacact tttagtacaa tggagtggct gagcctttga gcacaccacc	480
attacatcat cgtggcaaat taaagaagga ggtgggaaaa gaggacttat tgttgtc	537
atg gcc cat gag atg att gga act caa att gtt act gag agg ttg gtg	595
Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val	
1 5 10 15	
gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat agc cgg	633
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg	
20 25 30	
cca ttt gtg gaa tac aat aca tcc cac att ttg gaa gcc att aat atc	691
Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile	
35 40 45	
aac tgc tcc aag ctt atg aag cga agg ttg caa cag gac aaa gtg tta	729
Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu	
50 55 60	
att aca gag ctg atc cag cat tca gcg aaa cat aag gtt gac att gat	777
Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp	
65 70 75 80	
tgc agt cag aag gtt gta gtt tac gat caa agc tcc caa gat gtt gcc	825
Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala	
85 90 95	
tct ctg tct tca gac tgt ttt ctg act gta ctt ctg ggt aaa ctg gag	873
Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu	
100 105 110	
aag agc ttc aac tct gtt cac ctg ctt gca ggt ggg ttt gct gag ttc	921
Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe	
115 120 125	
tct cgt tgt ttc cct ggc ctg tgt gaa gga aaa tcc act cta gtc cct	959
Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro	
130 135 140	
acc tgc att tct cag cct tgc tta cct gtt gcc aac att ggg cca acc	1017
Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr	
145 150 155 160	
cga att ctt ccc aat ctt tat ctt ggc tgc cag cga gat gtc ctg aac	1055
Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn	

165	170	175	
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gcc tac atc atg aag agg atg gac atg tct tta gat gaa gct tac aga Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg 260 265 270			1353
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ctg tcc gca gac agg ctg gaa gac agc aat aag ctc aag cgt tcc ttc Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe 385 390 395 400			1737

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tcc act act ctg gat ggg acc aac aag cta tgc cag ttc tcc cct gtt Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val 435 440 445	1881
cag gaa cta tgc gag cag act ccc gaa acc agt cct gat aag gag gaa Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu 450 455 460	1929
gcc agc atc ccc aag aag ctg cag acc gcc agg cct tca gac agc cag Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln 465 470 475 480	1977
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tgc cgg cgg agc tgg cat gaa gag agc ccc ttt gaa aag cag ttt aaa Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys 610 615 620	2409

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Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn	
625 630 635 640	
agg tca cgg gaa gag ctg ggg aaa gtg ggc agt cag tct agc ttt tgg	2505
Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser	
645 650 655	
ggc agc atg gaa atc att gag gtc tcc tgagaagaaa gacacttgty	2553
Gly Ser Met Glu Ile Ile Glu Val Ser	
660 665	
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gatggagata attttttttt cttctcagct ttatgaagag aaggggaaact gtctaggatt	3332
cagctgaacc accaggaacc tggcaacatc acgatttaag ctaagggttg gaggctaacg	3392
agtctacctc cctcttttga aatcaaagaa ttgtttaaaa tgggattgtc aatcctttaa	3452
ataaagatga acttggtttc aagccaaatg tgaatttatt tgggttggtg gcagagcagc	3512
agcaccttca aattctcagc caaagcagat gttttttgcc tttctgcttc actgcattga	3572
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agtggctttt atccctctgg catgcgatgg ggcctgatgtt tctatgattg cctcagactt	3752
tcacatttac tagtagggct gagagaggct ttagttagga aggaatattc agaataaaac	3812
ggttgagaaa gctgagaaga ccattgagtt ttgatcagtt gtgaatagag tgcaaaagcca	3872
tggccaaagct gttttttggaa acgctggcgg gcggtgtcttc agtggaaaaa gaaatcaaa	3932

atggagcgag agcaaaagggg cgtcctcagt cctcaacctt caatcactgt atggaatcgg	3992
tcttggcagc tgaacatagg aggtcactgg aacaagtgat agtgcagatt ggcttttcaaa	4052
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acaacagcag ctttttgggg gtgggggtgg gcgggtgttg tcattgttct ttccttctct	4172
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atgatatgac tcaacacaga ccgacttggg tatgggggatg atgagccgca cagacctcac	4352
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taagaaagga aagcagtagc tccttgctaa cgatgtttca ggaggtttg ggcaacttggg	4652
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gatgtcttta ggtgggggtg tggttggtc tcttcagcat gtaattgggg aaacctcgc	4892
gtctactagg ggtgatacag atggtgattt taaagagcaa aactagactt ctatgtgaga	4952
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aggatttagc tcaaaataaa gtggtggtgt catcaggttt attccgtgtt ctgtcattca	5312
catggaaac cggtatgatta gctaacagtt tagtgccagc cttcattctt tactgtgtac	5372
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gattccagaa cacacaag	5450

<210> 109
 <211> 665
 <212> PRT

<213> Homo sapiens

<400> 109

Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val
1 5 10 15

Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg
20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile
35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu
50 55 60

Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp
65 70 75 80

Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala
85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu
100 105 110

Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe
115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro
130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr
145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn
165 170 175

Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser
180 185 190

Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg
195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp

210

215

220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val
 225 230 235 240

Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu
 275 280 285

Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala
 290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn
 305 310 315 320

Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro
 325 330 335

Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln
 340 345 350

Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro
 355 360 365

Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His
 370 375 380

Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe
 385 390 395 400

Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser
 405 410 415

Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro
 420 425 430

Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val
 435 440 445

Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu
 450 455 460

Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln
 465 470 475 480

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln
 485 490 495

Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn
 500 505 510

Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu
 515 520 525

Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu
 530 535 540

Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala
 545 550 555 560

Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser
 565 570 575

Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp
 580 585 590

Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp
 595 600 605

Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys
 610 615 620

Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn
 625 630 635 640

Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser
 645 650 655

Gly Ser Met Glu Ile Ile Glu Val Ser
 660 665

<210> 110
 <211> 625
 <212> PRT
 <213> Homo sapiens

<400> 110

Met	Ala	Gly	Asp	Arg	Leu	Pro	Arg	Lys	Val	Met	Asp	Ala	Lys	Lys	Leu
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Ala	Ser	Leu	Leu	Arg	Gly	Gly	Pro	Gly	Gly	Pro	Leu	Val	Ile	Asp	Ser
		20					25						30		
Arg	Ser	Phe	Val	Glu	Tyr	Asn	Ser	Trp	His	Val	Leu	Ser	Ser	Val	Asn
		35					40					45			
Ile	Cys	Cys	Ser	Lys	Leu	Val	Lys	Arg	Arg	Leu	Gln	Gln	Gly	Lys	Val
	50					55					60				
Thr	Ile	Ala	Glu	Leu	Ile	Gln	Pro	Ala	Ala	Arg	Ser	Gln	Val	Glu	Ala
65					70					75				80	
Thr	Glu	Pro	Gln	Asp	Val	Val	Val	Tyr	Asp	Gln	Ser	Thr	Arg	Asp	Ala
			35						90					95	
Ser	Val	Leu	Ala	Ala	Asp	Ser	Phe	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Leu
		100						105					110		
Asp	Gly	Cys	Phe	Asp	Ser	Val	Ala	Ile	Leu	Thr	Gly	Gly	Phe	Ala	Thr
	115						120					125			
Phe	Ser	Ser	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Pro	Ala	Ala	Leu
	130					135					140				
Leu	Pro	Met	Ser	Leu	Ser	Gln	Pro	Cys	Leu	Pro	Val	Pro	Ser	Val	Gly
145					150					155					160
Leu	Thr	Arg	Ile	Leu	Pro	His	Leu	Tyr	Leu	Gly	Ser	Gln	Lys	Asp	Val
			165						170					175	
Leu	Asn	Lys	Asp	Leu	Met	Thr	Gln	Asn	Gly	Ile	Ser	Tyr	Val	Leu	Asn
		180						185					190		
Ala	Ser	Asn	Ser	Cys	Pro	Lys	Pro	Asp	Phe	Ile	Cys	Glu	Ser	Arg	Phe
		195					200					205			
Met	Arg	Val	Pro	Ile	Asn	Asp	Asn	Tyr	Cys	Glu	Lys	Leu	Leu	Pro	Trp
	210					215					220				
Leu	Asp	Lys	Ser	Ile	Glu	Phe	Ile	Asp	Lys	Ala	Lys	Leu	Ser	Ser	Cys
225					230					235					240
Gln	Val	Ile	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile
			245						250					255	
Ala	Ile	Ala	Tyr	Ile	Met	Lys	Thr	Met	Gly	Met	Ser	Ser	Asp	Asp	Ala

260					265					270						
Tyr	Arg	Phe	Val	Lys	Asp	Arg	Arg	Pro	Ser	Ile	Ser	Pro	Asn	Phe	Asn	
275					280					285						
Phe	Leu	Gly	Gln	Leu	Leu	Glu	Tyr	Glu	Arg	Thr	Leu	Lys	Leu	Leu	Ala	
290					295					300						
Ala	Leu	Gln	Gly	Asp	Pro	Gly	Thr	Pro	Ser	Gly	Thr	Pro	Glu	Pro	Pro	
305					310					315					320	
Pro	Ser	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Pro	Arg	Leu	Pro	Pro	Pro	Thr	
325					330					335						
Ser	Glu	Ser	Ala	Ala	Thr	Gly	Asn	Ala	Ala	Ala	Arg	Glu	Gly	Gly	Leu	
340					345					350						
Ser	Ala	Gly	Gly	Glu	Pro	Pro	Ala	Pro	Pro	Thr	Pro	Pro	Ala	Thr	Ser	
355					360					365						
Ala	Leu	Gln	Gln	Gly	Leu	Arg	Gly	Leu	His	Leu	Ser	Ser	Asp	Arg	Leu	
370					375					380						
Gln	Asp	Thr	Asn	Arg	Leu	Lys	Arg	Ser	Phe	Ser	Leu	Asp	Ile	Lys	Ser	
385					390					395					400	
Ala	Tyr	Ala	Pro	Ser	Arg	Arg	Pro	Asp	Gly	Pro	Gly	Pro	Pro	Asp	Pro	
405					410					415						
Gly	Glu	Ala	Pro	Lys	Leu	Cys	Lys	Leu	Asp	Ser	Pro	Ser	Gly	Ala	Ala	
420					425					430						
Leu	Gly	Leu	Ser	Ser	Pro	Ser	Pro	Asp	Ser	Pro	Asp	Ala	Ala	Pro	Glu	
435					440					445						
Ala	Arg	Pro	Arg	Pro	Arg	Arg	Arg	Pro	Arg	Pro	Pro	Ala	Gly	Ser	Pro	
450					455					460						
Ala	Arg	Ser	Pro	Ala	His	Ser	Leu	Gly	Leu	Asn	Phe	Gly	Asp	Ala	Ala	
465					470					475					480	
Arg	Gln	Thr	Pro	Arg	His	Gly	Leu	Ser	Ala	Leu	Ser	Ala	Pro	Gly	Leu	
485					490					495						
Pro	Gly	Pro	Gly	Gln	Pro	Ala	Gly	Pro	Gly	Ala	Trp	Ala	Pro	Pro	Leu	
500					505					510						
Asp	Ser	Pro	Gly	Thr	Pro	Ser	Pro	Asp	Gly	Pro	Trp	Cys	Phe	Ser	Pro	
515					520					525						
Glu	Gly	Ala	Gln	Gly	Ala	Gly	Gly	Val	Leu	Phe	Ala	Pro	Phe	Gly	Arg	
530					535					540						
Ala	Gly	Ala	Pro	Gly	Pro	Gly	Gly	Gly	Ser	Asp	Leu	Arg	Arg	Arg	Glu	
545					550					555					560	
Ala	Ala	Arg	Ala	Glu	Pro	Arg	Asp	Ala	Arg	Thr	Gly	Trp	Pro	Glu	Glu	

565	570	575
Pro Ala Pro Glu Thr Gln Phe Lys Arg Arg Ser Cys Gln Met Glu Phe		
580	585	590
Glu Glu Gly Met Val Glu Gly Arg Ala Arg Gly Glu Glu Leu Ala Ala		
595	600	605
Leu Gly Lys Gln Ala Ser Phe Ser Gly Ser Val Glu Val Ile Glu Val		
610	615	620
Ser		
625		
<210> 111		
<211> 381		
<212> PRT		
<213> Homo sapiens		
<400> 111		
Met Ile Asp Thr Leu Arg Pro Val Pro Phe Ala Ser Glu Met Ala Ile		
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Ser Lys Thr Val Ala Trp Leu Asn Glu Gln Leu Glu Leu Gly Asn Glu		
20	25	30
Arg Leu Leu Leu Met Asp Cys Arg Pro Gln Glu Leu Tyr Glu Ser Ser		
35	40	45
His Ile Glu Ser Ala Ile Asn Val Ala Ile Pro Gly Ile Met Leu Arg		
50	55	60
Arg Leu Gln Lys Gly Asn Leu Pro Val Arg Ala Leu Phe Thr Arg Gly		
65	70	75
Glu Asp Arg Asp Arg Phe Thr Arg Arg Cys Gly Thr Asp Thr Val Val		
85	90	95
Leu Tyr Asp Glu Ser Ser Ser Asp Trp Asn Glu Asn Thr Gly Gly Glu		
100	105	110
Ser Leu Leu Gly Leu Leu Leu Lys Lys Leu Lys Asp Glu Gly Cys Arg		
115	120	125
Ala Phe Tyr Leu Glu Gly Gly Phe Ser Lys Phe Gln Ala Glu Phe Ser		
130	135	140
Leu His Cys Glu Thr Asn Leu Asp Gly Ser Cys Ser Ser Ser Ser Pro		
145	150	155
Pro Leu Pro Val Leu Gly Leu Gly Gly Leu Arg Ile Ser Ser Asp Ser		
165	170	175
Ser Ser Asp Ile Glu Ser Asp Leu Asp Arg Asp Pro Asn Ser Ala Thr		
180	185	190

Asp Ser Asp Gly Ser Pro Leu Ser Asn Ser Gln Pro Ser Phe Pro Val
 195 200 205

Glu Ile Leu Pro Phe Leu Tyr Leu Gly Cys Ala Lys Asp Ser Thr Asn
 210 215 220

Leu Asp Val Leu Glu Glu Phe Gly Ile Lys Tyr Ile Leu Asn Val Thr
 225 230 235 240

Pro Asn Leu Pro Asn Leu Phe Glu Asn Ala Gly Glu Phe Lys Tyr Lys
 245 250 255

Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Gln Phe Phe
 260 265 270

Pro Glu Ala Ile Ser Phe Ile Asp Glu Ala Arg Gly Lys Asn Cys Gly
 275 280 285

Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Val Thr Val Thr
 290 295 300

Val Ala Tyr Leu Met Gln Lys Leu Asn Leu Ser Met Asn Asp Ala Tyr
 305 310 315 320

Asp Ile Val Lys Met Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe
 325 330 335

Met Gly Gln Leu Leu Asp Phe Glu Arg Thr Leu Gly Leu Ser Ser Pro
 340 345 350

Cys Asp Asn Arg Val Pro Ala Gln Gln Leu Tyr Phe Thr Thr Pro Ser
 355 360 365

Asn Gln Asn Val Tyr Gln Val Asp Ser Leu Gln Ser Thr
 370 375 380

<210> 112
 <211> 482
 <212> PRT
 <213> Homo sapiens
 <400> 112

Met Pro Pro Ser Pro Leu Asp Asp Arg Val Val Val Ala Leu Ser Arg
 1 5 10 15

Pro Val Arg Pro Gln Asp Leu Asn Leu Cys Leu Asp Ser Ser Tyr Leu
 20 25 30

Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr
 35 40 45

Thr Val Val Ser Leu Lys Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser
 50 55 60

Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys
 65 70 75 80

Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala
 85 90 95
 Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys
 100 105 110
 Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser
 115 120 125
 Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu
 130 135 140
 Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr
 145 150 155 160
 Lys Cys Ser Lys Ser His Leu Pro Ser Gln Gly Pro Val Ile Ile Asp
 165 170 175
 Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gln Gly Ala Val
 180 185 190
 His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly
 195 200 205
 Lys Ile Thr Val Leu Asp Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser
 210 215 220
 Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr
 225 230 235 240
 Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu
 245 250 255
 Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly
 260 265 270
 Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu
 275 280 285
 Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Gly Ala Ser Ala Ala Ser
 290 295 300
 Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala
 305 310 315 320
 Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp
 325 330 335
 Ala Gln Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile
 340 345 350
 Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe
 355 360 365
 Asn Tyr Lys Arg Leu Pro Ala Thr Asp Ser Asn Lys Gln Asn Leu Arg
 370 375 380

Gln Tyr Phe Glu Glu Ala Phe Glu Phe Ile Glu Glu Ala His Gln Cys
 385 390 395 400
 Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala
 405 410 415
 Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr
 420 425 430
 Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn
 435 440 445
 Leu Asn Phe Met Gly Gln Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn
 450 455 460
 Gly Val Thr Pro Arg Ile Leu Thr Pro Lys Leu Met Gly Val Glu Thr
 465 470 475 480
 Val Val

<210> 113
 <211> 2756
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (369)..(2348)

<400> 113
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 atgaatctag tgtgaggggc tgctttgtgg aaggaatcct ttgcaagagc atatcaacag 180
 gaaagagaaa gagacattca gttggagggc tcttgctgaa atggatttaa ctctcctctt 240
 gccagtcacc actagcctga cctcatacat ttttagtaca atggagtggc tgagcctttg 300
 agcacagcac cattacatca tcgtggcaaa ttaaagaacg aggtggggaa agaggactta 360
 ttgttgtc atg gcc cat gag atg att gga act caa att gtt act gag agc 410
 Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Ser
 1 5 10
 ttg gtg gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat 453
 Leu Val Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp
 15 20 25 30
 agc cga cca ttt gtg gaa tac aat acg tct cac att ttg gaa gcc att 506
 Ser Arg Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile
 35 40 45
 aat atc aac tgc tcc aaa ctg atg aag cga agg ttg caa cag gac aaa 554

Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys	
50 55 60	
gta tta att aca gaa cta atc cac caa tct aca aag cat aag gtt gac	692
Val Leu Ile Thr Glu Leu Ile His Gln Ser Thr Lys His Lys Val Asp	
65 70 75	
att gac tgc aat caa aga gtg gta gtt tat gat cac agt tca caa gat	650
Ile Asp Cys Asn Gln Arg Val Val Val Tyr Asp His Ser Ser Gln Asp	
80 85 90	
gtt ggt tct ctg tct tca gac tgc ttt ctc act gta ctt ctg ggt aag	693
Val Gly Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys	
95 100 105 110	
ctg gag aga agc ttc aac tct gtc cac ctg ctt gca ggt ggc ttt gct	746
Leu Glu Arg Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala	
115 120 125	
gag ttc tct cgt tgt ttc cct ggc ctc tgt gaa gga aag tcc act cta	794
Glu Phe Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu	
130 135 140	
gtc cct acc tgc ata tct cag cct tgc tta cct gtt gcg aac att ggg	842
Val Pro Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly	
145 150 155	
cca act cga att ctt ccc aat ctc tat ctt ggc tgc cag cga gat gtc	890
Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val	
160 165 170	
ctc aac aag gac ctg atg caa cag aat ggg att ggc tat gtg tta aat	938
Leu Asn Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn	
175 180 185 190	
gcc agc aat acc tgt cca aag cct gac ttc ata cct gaa tct cac ttc	986
Ala Ser Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe	
195 200 205	
ctg cga gtg cct gtg aat gac agc ttt tgt gag aaa atc cta cca tgg	1034
Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp	
210 215 220	
ttg gac aag tct gtg gat ttc att gag aaa gca aaa gcc tcc aat ggc	1082
Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly	
225 230 235	
tgt gtg ctt atc cac tgc tta gct ggg atc tct cgc tcc gcc act att	1130
Cys Val Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile	
240 245 250	
gct att gcc tac atc atg aag agg atg gac atg tct cta gat gag gct	1178
Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala	
255 260 265 270	
tac aga ttt gtg aaa gaa aaa aga cct act ata tct ccg aat ttt aat	1226
Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn	

275	280	285	
ttt atg ggc caa ctc atg gac tat	gag aag acg att aat aac cag act	1274	
Phe Met Gly Gln Leu Met Asp Tyr	Glu Lys Thr Ile Asn Asn Gln Thr		
290	295 300		
gga atg tca ggg cca aag agc aaa ctg aag ctg ctg cac cta gac aaa	1322		
Gly Met Ser Gly Pro Lys Ser Lys	Leu Lys Leu Leu His Leu Asp Lys		
305	310 315		
ccc agt gag ccc gtg cct gca gcc tca gag ggc gga tgg aag agt gca	1370		
Pro Ser Glu Pro Val Pro Ala Ala Ser Glu Gly Gly Trp Lys Ser Ala			
320	325 330		
ctg tct ctc agt cca ccc tgt gcc aac tcg acc tcg gag gca tca ggg	1413		
Leu Ser Leu Ser Pro Pro Cys Ala Asn Ser Thr Ser Glu Ala Ser Gly			
335	340 345 350		
caa agg ctt gtg cat cct gca agt gtg ccc cgc tta cag ccg tca ctc	1466		
Gln Arg Leu Val His Pro Ala Ser Val Pro Arg Leu Gln Pro Ser Leu			
355	360 365		
tta gag gac agt ccg ctg gta cag gcg ctc agt ggg ctc cag ctg tcc	1514		
Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu Gln Leu Ser			
370	375 380		
tca gag aag ctg gaa gac agc act aag ctc aag cgt tcc ttc tct ctc	1562		
Ser Glu Lys Leu Glu Asp Ser Thr Lys Leu Lys Arg Ser Phe Ser Leu			
385	390 395		
gat atc aaa tct gtt tca tat tca gcc agt atg gcc gcg tcc cta cac	1610		
Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu His			
400	405 410		
ggc ttc tcg tca gag gag gct tta gac tac tgc aaa cct tct gcc aca	1653		
Gly Phe Ser Ser Glu Glu Ala Leu Asp Tyr Cys Lys Pro Ser Ala Thr			
415	420 425 430		
ctg gat ggg acc aac aag ctc tgc cag ttc tcc ccc gtt cag gag gta	1706		
Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln Glu Val			
435	440 445		
tca gaa cag agt cca gag acc agc ccg gat aag gag gag gcc cac atc	1754		
Ser Glu Gln Ser Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala His Ile			
450	455 460		
ccc aag cag ccc caa cct ccc agg cct tct gag agc cag gtc aca cgc	1802		
Pro Lys Gln Pro Gln Pro Pro Arg Pro Ser Glu Ser Gln Val Thr Arg			
465	470 475		
ttg cac tca gtg aga acc ggc agt agt ggg tcc acc cag agg ccc ttc	1850		
Leu His Ser Val Arg Thr Gly Ser Ser Gly Ser Thr Gln Arg Pro Phe			
480	485 490		
ttc tcg cca ctg cat cgg agc ggg agt gta gag gac aat tac cat acc	1898		
Phe Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr His Thr			
495	500 505 510		

aac ttc ctt ttt ggc ctt tcc acc agc cag caa cac ctc acc aag tct Asn Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr Lys Ser 515 520 525	1946
gca ggg ctt ggc ctc aag ggc tgg cac tca gat att ctg gct ccc cag Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala Pro Gln 530 535 540	1994
tcc tct gcc ccc tcc ctg acc agc agt tgg tat ttt gct acg gag cct Ser Ser Ala Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr Glu Pro 545 550 555	2042
tca cac ttg tac tct gct tca gcc atc tat gga ggc aac agc agt tac Ser His Leu Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Asn Ser Ser Tyr 560 565 570	2090
tct gcc tac agc tgt ggc cag ctg ccc act tgc agt gac caa atc tat Ser Ala Tyr Ser Cys Gly Gln Leu Pro Thr Cys Ser Asp Gln Ile Tyr 575 580 585 590	2138
tct gtt cgt agg cgg cag aag cct act gac aga gct gac tcg agg cgg Ser Val Arg Arg Arg Gln Lys Pro Thr Asp Arg Ala Asp Ser Arg Arg 595 600 605	2186
agc tgg cat gaa gag agc ccc ttt gaa aag cag ttt aaa cgc aga agc Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg Arg Ser 610 615 620	2234
tgc caa atg gaa ttt gga gag agc att atg tgc gag aac agg tcc agg Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg Ser Arg 625 630 635	2282
gag gag ctg ggc aag gtg ggc agc cag tcc agc ttc tcc ggc agc atg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly Ser Met 640 645 650	2330
gag atc atc gag gtc tct tgagaagacc tcgtcgttcc tgttgacagt Glu Ile Ile Glu Val Ser 655 660	2378
tttgtttcct gttcacaaaa aatagtcctt gtaaactctga aatatgtata tgtacataca	2438
tatatatattt tggaatatag agctacggtta taaaagcaac agatggatca acacagttgt	2498
tctctcagca cctgcactga gaatagctaa ctctcagaaa agattggaag ggtagatggt	2558
agaattctcc cagccaggag aagagatttg gttcagtga ttgcacatct tcttgttcct	2618
acaaaaagcaa gggttttggt tgtttgtatg ttgtttgttt ttaatgtag agggcaaaat	2678
ccctccatt ttcacgtgca acagaggtct cagaactcat ctctgtccag gcccttcct	2738
agtgcacctt agcgctaa	2756

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<211> 660
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 <213> Mus musculus

<400> 114

Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Ser Leu Val
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Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg
 20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile
 35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu
 50 55 60

Ile Thr Glu Leu Ile His Gln Ser Thr Lys His Lys Val Asp Ile Asp
 65 70 75 80

Cys Asn Gln Arg Val Val Val Tyr Asp His Ser Ser Gln Asp Val Gly
 85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu
 100 105 110

Arg Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe
 115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro
 130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr
 145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn
 165 170 175

Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser
 180 185 190

Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg
 195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp
 210 215 220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val
 225 230 235 240

Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Met
 275 280 285

Gly Gln Leu Met Asp Tyr Glu Lys Thr Ile Asn Asn Gln Thr Gly Met
 290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Asp Lys Pro Ser
 305 310 315 320

Glu Pro Val Pro Ala Ala Ser Glu Gly Gly Trp Lys Ser Ala Leu Ser
 325 330 335

Leu Ser Pro Pro Cys Ala Asn Ser Thr Ser Glu Ala Ser Gly Gln Arg
 340 345 350

Leu Val His Pro Ala Ser Val Pro Arg Leu Gln Pro Ser Leu Leu Glu
 355 360 365

Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu Gln Leu Ser Ser Glu
 370 375 380

Lys Leu Glu Asp Ser Thr Lys Leu Lys Arg Ser Phe Ser Leu Asp Ile
 385 390 395 400

Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu His Gly Phe
 405 410 415

Ser Ser Glu Glu Ala Leu Asp Tyr Cys Lys Pro Ser Ala Thr Leu Asp
 420 425 430

Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln Glu Val Ser Glu
 435 440 445

Gln Ser Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala His Ile Pro Lys
 450 455 460

Gln Pro Gln Pro Pro Arg Pro Ser Glu Ser Gln Val Thr Arg Leu His
 465 470 475 480

Ser Val Arg Thr Gly Ser Ser Gly Ser Thr Gln Arg Pro Phe Phe Ser
 485 490 495

Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr His Thr Asn Phe
 500 505 510

Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr Lys Ser Ala Gly
 515 520 525

Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala Pro Gln Ser Ser
 530 535 540

Ala Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr Glu Pro Ser His
 545 550 555 560

Leu Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Asn Ser Ser Tyr Ser Ala
 565 570 575

Tyr Ser Cys Gly Gln Leu Pro Thr Cys Ser Asp Gln Ile Tyr Ser Val
 580 585 590

Arg Arg Arg Gln Lys Pro Thr Asp Arg Ala Asp Ser Arg Arg Ser Trp
 595 600 605

His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg Arg Ser Cys Gln
 610 615 620

Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu
 625 630 635 640

Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly Ser Met Glu Ile
 645 650 655

Ile Glu Val Ser

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 <212> DNA
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 tgttactgag aggttggtgg ctctgctgga aagtggaaacg gaaaaagtgc tgctaattga 180
 tagccggcca tttgtggaat acaatacatc ccacattttg gaagccatta atatcaactg 240
 ctccaagcct atgaagcgaa ggttgcaaca ggacaaagtg ttaattacag agctcatcca 300
 gcattcagcg aaacataagg ttgacattga ttgcagtcag aaggttgtag ttacgatca 360
 aagctcccaa gatgttgccct ctctctcttc agactgtttt ctcaactgt 408

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 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 116
 Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala Leu Leu
 1 5 10

<210> 117
 <211> 13
 <212> PRT
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<400> 117
 Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp
 1 5 10

<210> 118
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 118
 Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile
 1 5 10

<210> 119
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 <212> PRT

<210> Homo sapiens

<400> 119

Val Asp Ile Asp Cys Ser Gln Lys Val Val Val Tyr Asp
1 5 10

<210> 120

<211> 13

<212> PFT

<213> Homo sapiens

<400> 120

Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe
1 5 10

<210> 121

<211> 13

<212> PFT

<213> Homo sapiens

<400> 121

Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser
1 5 10

<210> 122

<211> 13

<212> PFT

<213> Homo sapiens

<400> 122

Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln
1 5 10

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<400> 123

Pro Ser Asp Ser Gln Ser Lys Arg Leu His Ser Val Arg
1 5 10

<210> 124

<211> 13

<212> PFT

<213> Homo sapiens

<400> 124

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly
1 5 10

<210> 125
<211> 13
<212> PRT
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<400> 125

Gly Asp Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro
1 5 10

<210> 126
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<212> PRT
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<400> 126

Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser Arg Arg
1 5 10

<210> 127
<211> 13
<212> PRT
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<400> 127

Ser Asp Arg Ala Asp Ser Arg Arg Ser Trp His Glu Glu
1 5 10

<210> 128
<211> 14
<212> PRT
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<400> 128

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile
1 5 10

<210> 129
<211> 14
<212> PRT
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<400> 129

Glu Ala Ile Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg
1 5 10

<210> 130
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Ile Gly Tyr Val Leu Asn Ala Ser Tyr Thr Cys Pro Lys Pro
 1 5 10

<210> 131
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Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu
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<210> 132
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Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys
 1 5 10

<210> 133
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Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu Leu Gly Lys
 1 5 10

<210> 134
 <211> 140
 <212> PRT
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<400> 134

Gly Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp
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Val Leu Asn Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu
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Asn Ala Ser Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His
 35 40 45

Phe Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro
 50 55 60

Trp Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn
 65 70 75 80

Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr
 85 90 95

Ile Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu
 100 105 110

Ala Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe
 115 120 125

Asn Phe Leu Gly Gln Leu Leu Asp Tyr Glu Lys Lys
 130 135 140

<210> 135
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 <213> Mus musculus

<400> 135

Gly Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp
 1 5 10 15

Val Leu Asn Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu
 20 25 30

Asn Ala Ser Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His
 35 40 45

Phe Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro
 50 55 60

Trp Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn
 65 70 75 80

Gly Cys Val Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr
 85 90 95

Ile Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu
 100 105 110

Ala Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe
 115 120 125

Asn Phe Met Gly Gln Leu Met Asp Tyr Glu Lys Thr
 130 135 140

<210> 136
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 136
 gcagcagcgg ccgcattggg ccaaccgaa ttcttccc

38

<210> 137
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 137
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<210> 138
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 138
 gcagcagcgg ccgcatggcc catgagatga ttggaactc 39

<210> 139
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 139
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<210> 140
 <211> 38
 <212> DNA
 <213> Homo sapiens

<400> 140
 gcagcagcgg ccgcattggg ccaactcgaa ttcttccc 38

<210> 141
 <211> 37
 <212> DNA
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<400> 141
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<210> 142
 <211> 39
 <212> DNA
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<400> 142
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<210> 143
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 143
 gcagcagtcg accgtcttct catagtccat gagttgg 37

<210> 144
 <211> 2'
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 <213> Homo sapiens

<400> 144

Asn Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala
 1 5 10 15

Thr Ile Ala Ile Ala Tyr Ile
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<210> 145
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 <213> Homo sapiens

<400> 145
 cacaccacca ttacatcatc gtggc 25

<210> 146
 <211> 20
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<400> 146
 tgetgctctg ctaccaaccc 20

<210> 147
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 gtgacaactt tcgtttccct ctgagggaat tgggaggtcg ggggccccaa aagctttcag 180
 tccagtgtaa agctgttgga gcgcgggagc aaaggtaaag aatgatgtaa tgcgttggt 240
 gctccaaagc atcttttgtt gtggaatggt tattccagtc atctctttat gaatcaaatg 300
 tgaggggctg ctttgtggac ggagtccttt gcaagagcac atcaacggga aagagaaaga 360
 gacattcaact tggagggctc ttgctgaaaa tgggtttaac tctcttttg ccagtcacca 420

ccagcctgac ctcatacact tttagtacaa tggagtggtt gagcctttga gcacaccacc 480

attacatcat cgtggcacaat taaagaagga ggtgggaaaa gaggacttat tgttgtc 537

atg gcc cat gag atg att gga act caa att gtt act gag agg ttg gtg 585
Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val
1 5 10 15

gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat agc cgg 633
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg
20 25 30

cca ttt gtg gaa tac aat aca tcc cac att ttg gaa gcc att aat atc 681
Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile
35 40 45

aac tgc tcc aag ctt atg aag cga agg ttg caa cag gac aaa gtg tta 729
Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu
50 55 60

att aca gag ctc atc cag cat tca gcg aaa cat aag gtt gac att gat 777
Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp
65 70 75 80

tgc agt cag aag gtt gta gtt tac gat caa agc tcc caa gat gtt gcc 825
Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala
85 90 95

tct ctc tct tca gac tgt ttt ctc act gta ctt ctg ggt aaa ctg gag 873
Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu
100 105 110

aag agc ttc aac tct gtt cac ctg ctt gca ggt ggg ttt gct gag ttc 921
Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe
115 120 125

tct cgt tgt ttc cct ggc ctc tgt gaa gga aaa tcc act cta gtc cct 969
Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro
130 135 140

acc tgc att tct cag cct tgc tta cct gtt gcc aac att ggg cca acc 1017
Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr
145 150 155 160

cga att ctt ccc aat ctt tat ctt ggc tgc cag cga gat gtc ctc aac 1065
Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn
165 170 175

aag gag ctg ata cag cag aat ggg att ggt tat gtg tta aat gcc agc 1113
Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser
180 185 190

tat acc tgt cca aag cct gac ttt atc ccc gag tct cat ttc ctg cgt 1161
Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg
195 200 205

gtg cct gtg aat gac agc ttt tgt gag aaa att ttg ccg tgg ttg gac 1209

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp	
210 215 220	
aaa tca gta gat ttc att gag aaa gca aaa gcc tcc aat gga tgt gtt	1257
Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val	
225 230 235 240	
cta gtg cac tgt tta gct ggg atc tcc cgc tcc gcc acc atc gct atc	1305
Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile	
245 250 255	
gcc tac atc atg aag agg atg gac atg tct tta gat gaa gct tac aga	1353
Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg	
260 265 270	
ttt gtg aaa gaa aaa aga cct act ata tct cca aac ttc aat ttt ctg	1401
Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu	
275 280 285	
ggc caa ctc ctg gac tat gag aag aag att aag aac cag act gga gca	1449
Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala	
290 295 300	
tca ggg cca aag agc aaa ctc aag ctg ctg cac ctg gag aag cca aat	1497
Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn	
305 310 315 320	
gaa cct gtc cct gct gtc tca gag ggt gga cag aaa agc gag acg ccc	1545
Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro	
325 330 335	
ctc agt cca ccc tgt gcc gac tct gct acc tca gag gca gca gga caa	1593
Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln	
340 345 350	
agg ccc gtg cat ccc gcc agc gtg ccc agc gtg ccc agc gtg cag ccg	1641
Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro	
355 360 365	
tcg ctg tta gag gac agc ccg ctg gta cag gcg ctc agt ggg ctg cac	1689
Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His	
370 375 380	
ctg tcc gca gac agg ctg gaa gac agc aat aag ctc aag cgt tcc ttc	1737
Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe	
385 390 395 400	
tct ctg gat atc aaa tca gtt tca tat tca gcc agc atg gca gca tcc	1785
Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser	
405 410 415	
tta cat ggc ttc tcc tca tca gaa gat gct ttg gaa tac tac aaa cct	1833
Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro	
420 425 430	
tcc act act ctg gat ggg acc aac aag cta tgc cag ttc tcc cct gtt	1881
Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val	

435	440	445	
cag gaa cta tcy gag cag act ccc gaa acc agt cct gat aag gag gaa			1939
Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu			
450	455	460	
gcc agc atc ccc aag aag ctg cag acc gcc agg cct tca gac agc cag			1977
Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln			
465	470	475	480
agc aag cga ttg cat tcy gtc aga acc agc agc agt gcc acc gcc cag			2025
Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln			
485	490	495	
agg tcc ctt tta tct cca ctg cat cga agt ggg agc gtg gag gac aat			2073
Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn			
500	505	510	
tac cac acc agc ttc ctt ttc gcc ctt tcc acc agc cag cag cac ctc			2121
Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu			
515	520	525	
acg aag tct gct gcc ctg gcc ctt aag gcc tgg cac tcy gat atc ttg			2169
Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu			
530	535	540	
gcc ccc cag acc tct acc cct tcc ctg acc agc agc tgg tat ttt gcc			2217
Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala			
545	550	555	560
aca gag tcc tca cac ttc tac tct gcc tca gcc atc tac gga gcc agt			2265
Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser			
565	570	575	
gcc agt tac tct gcc tac agc tgc agc cag ctg ccc act tgc gga gac			2313
Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp			
580	585	590	
caa gtc tat tct gtg cgc agg cgg cag aag cca agt gac aga gct gac			2361
Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp			
595	600	605	
tcy cgg cgg agc tgg cat gaa gag agc ccc ttt gaa aag cag ttt aaa			2409
Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys			
610	615	620	
cgc aga agc tgc caa atg gaa ttt gga gag agc atc atg tca gag aac			2457
Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn			
625	630	635	640
agg tca cgg gaa gag ctg ggg aaa gtg gcc agt cag tct agc ttt tcy			2505
Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser			
645	650	655	
ggc agc atg gaa atc att gag gtc tcc tgagaagaaa gacacttggtg			2552
Gly Ser Met Glu Ile Ile Glu Val Ser			
660	665		

acttctatag acaatTTTTT ttttcttTgtt cacaaaaaaa ttcctgttaa atctgaaata	2612
tatatatgta catacatata tttttttTga aaatggagct atggtgtaaa agcaacaggt	2672
ggatcaacc agttgttact ctcttaacat ctgcatttga gagatcagct aatacttctc	2732
tcaacaaaaa tggaaggga gatgctagaa tccccctag acggaggaaa accattttat	2792
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485

490

495

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Lys Arg Arg Leu Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn	245	250	255
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Pro Ala His Tyr Gln Phe Leu Leu Asp Leu Gly Val Arg His Leu Val
25 30 35 40

tcc ctg acg gag cgc ggg ccc cct cac agc gac agc tgc ccc ggc ctc      256
Ser Leu Thr Glu Arg Gly Pro Pro His Ser Asp Ser Cys Pro Gly Leu
45 50 55

acc ctg cac cgc ctg cgc atc ccc gac ttc tgc ccg ccg gcc ccc gac      304
Thr Leu His Arg Leu Arg Ile Pro Asp Phe Cys Pro Pro Ala Pro Asp
60 65 70

cag atc gac cgc ttc gtg cag atc gtg gac gag gcc aac gca cgg gga      352
Gln Ile Asp Arg Phe Val Gln Ile Val Asp Glu Ala Asn Ala Arg Gly
75 80 85

gag gct gtg gga gtg cac tgt gct ctg ggc ttt ggc cgc act ggc acc      400
Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg Thr Gly Thr
90 95 100

atg ctg gcc tgt tac ctg gtg aag gag cgg ggc ttg gct gca gga gat      448
Met Leu Ala Cys Tyr Leu Val Lys Glu Arg Gly Leu Ala Ala Gly Asp
105 110 115 120

gcc att gct gaa atc cga cga cta cga ccc ggc tcc atc gag acc tat      496
Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Ser Ile Glu Thr Tyr
125 130 135

gag cag gag aaa gca gtc ttc cag ttc tac cag cga acg aaa      538
Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr Lys
140 145 150

taaggggact tagtaccctt ctaccaggcc ctcaactcccc tccccatgt tgcgatggg      598

gccagagatg aagggaagtg gactaaagta ttaaaccctc tagctcccat tggctgaaga      658

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cactgaagta gccacccct gcaggcaggt cctgattgaa ggggaggctt gtactgcttt 718
 gttgaataaa tgagttttac gaaccaggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 778
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 838
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc 878

<210> 152
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 152

Met Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu
 1 5 10 15

Ala Gly Leu Ala Leu Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu
 20 25 30

Asp Leu Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro
 35 40 45

His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro
 50 55 60

Asp Phe Cys Pro Pro Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile
 65 70 75 80

Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala
 85 90 95

Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys
 100 105 110

Glu Arg Gly Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu
 115 120 125

Arg Pro Gly Ser Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln
 130 135 140

Phe Tyr Gln Arg Thr Lys
 145 150

<210> 153

400> 153

108

Ser Pro Glu Pro Asp His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser
 275 280 285
 Phe Trp Ser Gln Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly
 290 295 300
 Ser Pro Ile His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly
 305 310 315 320
 Ala Phe Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser
 325 330 335
 Pro Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val
 340 345 350
 His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Gln
 355 360 365
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Lys Ala
 370 375 380
 Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Ser Glu Ala
 385 390 395 400
 Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Ala Arg Arg Ile
 405 410 415
 Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Val Glu Lys Glu Glu
 420 425 430
 Leu Lys Arg Lys Val Glu Met Trp Gln Lys Leu Asn Ser Arg Asp Gly
 435 440 445
 Ala Trp Glu Arg Ile Cys Gly Glu Arg Pro Phe Ile Leu Cys Ser Leu
 450 455 460
 Met Trp Ser Trp Val Glu
 465 470

<210> 154
 <211> 24
 <212> DNA
 <213> Homo sapiens

<400> 154
 tacaatttcg gatggaagga ttat

24

<210> 155
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 155
 gcatgacaat ggatagctac ttt

23

<210> 156
<211> 24
<212> DNA
<213> Homo sapiens

<400> 155
gagaaagcag tttccagtt ctac

24

<210> 157
<211> 24
<212> DNA
<213> Homo sapiens

<400> 157
atgggagcta gagggtttaa tact

24

<210> 158
<211> 14
<212> PRT
<213> Homo sapiens

<400> 158

Leu Thr Pro Leu Arg Asn Ile Ser Cys Cys Asp Pro Lys Ala
1 5 10

<210> 159
<211> 13
<212> PRT
<213> Homo sapiens

<400> 159

Thr Leu Ser Phe Trp Ser Gln Lys Phe Gly Gly Leu Glu
1 5 10

<210> 160
<211> 13
<212> PRT
<213> Homo sapiens

<400> 160

Val Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys
1 5 10

<210> 161
<211> 13
<212> PRT
<213> Homo sapiens

<400> 161

Pro Leu Asp Cys Gly Ser Ser Lys Ala Gln Phe Leu Val
1 5 10

<210> 162
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 162

Pro Thr Val Tyr Asn Thr Lys Lys Ile Phe Lys His Thr
 1 5 10

<210> 163
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 163

Gln Glu Gly Lys Val Ile His Cys His Ala Gly Leu Gly Arg Thr Gly
 1 5 10 15

Val Leu Ile Ala Tyr Leu Val
 20

<210> 164
 <211> 14
 <212> PRT
 <213> Homo sapiens

<400> 164

Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg
 1 5 10

<210> 165
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 165

His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro His Ser
 1 5 10

<210> 166
 <211> 23
 <212> PRT
 <213> Homo sapiens

<400> 166

Gly Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg Thr Gly
 1 5 10 15

Thr Met Leu Ala Cys Tyr Leu
 20

<210> 167
<211> 39
<212> DNA
<213> Homo sapiens

<400> 167
gcagcagcgg ccgcaatttc ggatggaagg attatggtg

39

<210> 168
<211> 33
<212> DNA
<213> Homo sapiens

<400> 168
gcagcagtcg acgaggccag gcttagggcc atc

33

<210> 169
<211> 38
<212> DNA
<213> Homo sapiens

<400> 169
gcagcagcgg ccgcatggag gctggcattt acttctac

38

<210> 170
<211> 35
<212> DNA
<213> Homo sapiens

<400> 170
gcagcagtcg accacccaag accacatcaa gctgc

35

<210> 171
<211> 39
<212> DNA
<213> Homo sapiens

<400> 171
gcagcagcgg ccgcctgttg gacctgggcg tgcggcacc

39

<210> 172
<211> 37
<212> DNA
<213> Homo sapiens

<400> 172
gcagcagtcg actttcgttc gctggtagaa ctggaag

37

<210> 173
<211> 38
<212> DNA

<213> Homo sapiens

<400> 173
gcagcagcgg ccgcatgggc gtgcagcccc ccaacttc

38

<210> 174
<211> 37
<212> DNA
<213> Homo sapiens

<400> 174
gcagcagtcg accaccaggt aacaggccag catggtg

37

<210> 175
<211> 806
<212> PRT
<213> Homo sapiens

<400> 175

Met	Gln	Val	Gln	Asp	Ala	Thr	Arg	Arg	Pro	Ser	Ala	Val	Arg	Phe	Leu
1				5					10					15	
Ser	Ser	Phe	Leu	Gln	Gly	Arg	Arg	His	Ser	Thr	Ser	Asp	Pro	Val	Leu
			20					25					30		
Arg	Leu	Gln	Gln	Ala	Arg	Arg	Gly	Ser	Gly	Leu	Gly	Ser	Gly	Ser	Ala
			35				40					45			
Thr	Lys	Leu	Leu	Ser	Ser	Ser	Ser	Leu	Gln	Val	Met	Val	Ala	Val	Ser
	50						55				60				
Ser	Val	Ser	His	Ala	Glu	Gly	Asn	Pro	Thr	Phe	Pro	Glu	Arg	Lys	Arg
65					70					75					80
Asn	Leu	Glu	Arg	Pro	Thr	Pro	Lys	Tyr	Thr	Lys	Val	Gly	Glu	Arg	Leu
				85					90					95	
Arg	His	Val	Ile	Pro	Gly	His	Met	Ala	Cys	Ser	Met	Ala	Cys	Gly	Gly
			100					105					110		
Arg	Ala	Cys	Lys	Tyr	Glu	Asn	Pro	Ala	Arg	Trp	Ser	Glu	Gln	Glu	Gln
			115				120					125			
Ala	Ile	Lys	Gly	Val	Tyr	Ser	Ser	Trp	Val	Thr	Asp	Asn	Ile	Leu	Ala
			130				135				140				
Met	Ala	Arg	Pro	Ser	Ser	Glu	Leu	Leu	Glu	Lys	Tyr	His	Ile	Ile	Asp
145					150					155					160
Gln	Phe	Leu	Ser	His	Gly	Ile	Lys	Thr	Ile	Ile	Asn	Leu	Gln	Arg	Pro
				165					170					175	
Gly	Glu	His	Ala	Ser	Cys	Gly	Asn	Pro	Leu	Glu	Gln	Glu	Ser	Gly	Phe
				180				185					190		

Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly Ile Tyr Phe Tyr Asn
 195 200 205
 Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu Thr Thr Ile Leu Asp
 210 215 220
 Met Val Lys Val Met Thr Phe Ala Leu Gln Glu Gly Lys Val Ala Ile
 225 230 235 240
 His Cys His Ala Gly Leu Gly Arg Thr Gly Val Leu Ile Ala Cys Tyr
 245 250 255
 Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln Ala Ile Ile Phe Val
 260 265 270
 Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg Gly Gln Leu Leu Cys
 275 280 285
 Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu Arg Asn Ile Phe Ser
 290 295 300
 Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu Pro Gln Tyr Leu Ile
 305 310 315 320
 Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala Arg Leu Leu Lys His
 325 330 335
 Val Pro Lys Ile Ile His Leu Val Cys Lys Leu Leu Leu Asp Leu Ala
 340 345 350
 Glu Asn Arg Pro Val Met Met Lys Asp Val Ser Glu Gly Pro Gly Leu
 355 360 365
 Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met Val Thr Met Gln Leu
 370 375 380
 Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val Ser Asn Pro Pro Asn
 385 390 395 400
 Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Phe Ser
 405 410 415
 Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg Arg Asn Val Glu Cys
 420 425 430
 Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu Ser Tyr Ser Asp Ser
 435 440 445
 Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln Gly Glu Thr Pro Gln
 450 455 460
 Thr Val Pro Ala Gln Ile Leu Val Gly His Lys Pro Arg Gln Gln Lys
 465 470 475 480
 Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro Glu Pro Asp Leu His
 485 490 495

Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe Trp Ser Gln Ser Lys
 500 505 510
 Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly Ser Pro Ile Phe His
 515 520 525
 Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly Ala Phe Ser Ala
 530 535 540
 Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser Pro Ser Phe
 545 550 555 560
 Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val Ser His
 565 570 575
 Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Arg Gln
 580 585 590
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Pro Lys
 595 600 605
 Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Leu Ser
 610 615 620
 Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Glu Ala
 625 630 635 640
 Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Ser Val
 645 650 655
 Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met Trp Gln Lys Glu Leu
 660 665 670
 Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys Gly Glu Arg Asp Pro
 675 680 685
 Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val Glu Gln Leu Lys Glu
 690 695 700
 Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu Val Asp Arg Arg Ala
 705 710 715 720
 Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys Gly Gln His Gln Thr
 725 730 735
 Ile Leu Cys Val Leu His Cys Ile Val Asn Leu Gln Thr Ile Pro Val
 740 745 750
 Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile Lys Ala Phe Thr Lys
 755 760 765
 Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val Tyr Asn Thr Leu Lys
 770 775 780
 Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg Lys Met Thr Lys Asp
 785 790 795 800

Gly Pro Lys Pro Gly Leu
805

<210> 176
<211> 747
<212> PRT
<213> Homo sapiens

<400> 176

Met	Val	Ala	Val	Ser	Ser	Val	Ser	His	Ala	Glu	Gly	Asn	Pro	Thr	Phe	1	5	10	15
Pro	Glu	Arg	Lys	Arg	Asn	Leu	Glu	Arg	Pro	Thr	Pro	Lys	Tyr	Thr	Lys	20	25	30	
Val	Gly	Glu	Arg	Leu	Arg	His	Val	Ile	Pro	Gly	His	Met	Ala	Cys	Ser	35	40	45	
Met	Ala	Cys	Gly	Gly	Arg	Ala	Cys	Lys	Tyr	Glu	Asn	Pro	Ala	Arg	Trp	50	55	60	
Ser	Glu	Gln	Glu	Gln	Ala	Ile	Lys	Gly	Val	Tyr	Ser	Ser	Trp	Val	Thr	65	70	75	80
Asp	Asn	Ile	Leu	Ala	Met	Ala	Arg	Pro	Ser	Ser	Glu	Leu	Leu	Glu	Lys	85	90	95	
Tyr	His	Ile	Ile	Asp	Gln	Phe	Leu	Ser	His	Gly	Ile	Lys	Thr	Ile	Ile	100	105	110	
Asn	Leu	Gln	Arg	Pro	Gly	Glu	His	Ala	Ser	Cys	Gly	Asn	Pro	Leu	Glu	115	120	125	
Gln	Glu	Ser	Gly	Phe	Thr	Tyr	Leu	Pro	Glu	Ala	Phe	Met	Glu	Ala	Gly	130	135	140	
Ile	Tyr	Phe	Tyr	Asn	Phe	Gly	Trp	Lys	Asp	Tyr	Gly	Val	Ala	Ser	Leu	145	150	155	160
Thr	Thr	Ile	Leu	Asp	Met	Val	Lys	Val	Met	Thr	Phe	Ala	Leu	Gln	Glu	165	170	175	
Gly	Lys	Val	Ala	Ile	His	Cys	His	Ala	Gly	Leu	Gly	Arg	Thr	Gly	Val	180	185	190	
Leu	Ile	Ala	Cys	Tyr	Leu	Val	Phe	Ala	Thr	Arg	Met	Thr	Ala	Asp	Gln	195	200	205	
Ala	Ile	Ile	Phe	Val	Arg	Ala	Lys	Arg	Pro	Asn	Ser	Ile	Gln	Thr	Arg	210	215	220	
Gly	Gln	Leu	Leu	Cys	Val	Arg	Glu	Phe	Thr	Gln	Phe	Leu	Thr	Pro	Leu	225	230	235	240
Arg	Asn	Ile	Phe	Ser	Cys	Cys	Asp	Pro	Lys	Ala	His	Ala	Val	Thr	Leu				

245	250	255
Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala 260 265 270		
Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu Val Cys Lys Leu 275 280 285		
Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met Lys Asp Val Ser 290 295 300		
Glu Gly Pro Gly Leu Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met 305 310 315 320		
Val Thr Met Gln Leu Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val 325 330 335		
Ser Asn Pro Pro Asn Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg 340 345 350		
Gly Met Ile Phe Ser Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg 355 360 365		
Arg Asn Val Glu Cys Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu 370 375 380		
Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln 385 390 395 400		
Gly Glu Thr Pro Gln Thr Val Pro Ala Gln Ile Leu Val Gly His Lys 405 410 415		
Pro Arg Gln Gln Lys Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro 420 425 430		
Glu Pro Asp Leu His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe 435 440 445		
Trp Ser Gln Ser Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly 450 455 460		
Ser Pro Ile Phe His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser 465 470 475 480		
Gly Ala Phe Ser Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro 485 490 495		
Val Ser Pro Ser Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His 500 505 510		
Gln Gln Val Ser His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro 515 520 525		
Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys 530 535 540		
Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp		

545 550 555 560
 Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu
 565 570 575
 Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn
 580 585 590
 Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met
 595 600 605
 Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys
 610 615 620
 Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val
 625 630 635 640
 Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu
 645 650 655
 Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys
 660 665 670
 Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys Ile Val Asn Leu
 675 680 685
 Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile
 690 695 700
 Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val
 705 710 715 720
 Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg
 725 730 735
 Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu
 740 745

 <210> 177
 <211> 699
 <212> PRT
 <213> Homo sapiens

 <400> 177
 Met Ala Cys Gly Gly Arg Ala Cys Lys Tyr Glu Asn Pro Ala Arg Trp
 1 5 10 15
 Ser Glu Gln Glu Gln Ala Ile Lys Gly Val Tyr Ser Ser Trp Val Thr
 20 25 30
 Asp Asn Ile Leu Ala Met Ala Arg Pro Ser Ser Glu Leu Leu Glu Lys
 35 40 45
 Tyr His Ile Ile Asp Gln Phe Leu Ser His Gly Ile Lys Thr Ile Ile
 50 55 60

Asn Leu Gln Arg Pro Gly Glu His Ala Ser Cys Gly Asn Pro Leu Glu
 65 70 75 80
 Gln Glu Ser Gly Phe Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly
 85 90 95
 Ile Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu
 100 105 110
 Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln Glu
 115 120 125
 Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly Val
 130 135 140
 Leu Ile Ala Cys Tyr Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln
 145 150 155 160
 Ala Ile Ile Phe Val Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg
 165 170 175
 Gly Gln Leu Leu Cys Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu
 180 185 190
 Arg Asn Ile Phe Ser Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu
 195 200 205
 Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala
 210 215 220
 Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu Val Cys Lys Leu
 225 230 235 240
 Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met Lys Asp Val Ser
 245 250 255
 Glu Gly Pro Gly Leu Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met
 260 265 270
 Val Thr Met Gln Leu Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val
 275 280 285
 Ser Asn Pro Pro Asn Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg
 290 295 300
 Gly Met Ile Phe Ser Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg
 305 310 315 320
 Arg Asn Val Glu Cys Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu
 325 330 335
 Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln
 340 345 350
 Gly Glu Thr Pro Gln Thr Val Pro Ala Gln Ile Leu Val Gly His Lys
 355 360 365

Pro Arg Gln Gln Lys Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro
 370 375 380
 Glu Pro Asp Leu His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe
 385 390 395 400
 Trp Ser Gln Ser Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly
 405 410 415
 Ser Pro Ile Phe His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser
 420 425 430
 Gly Ala Phe Ser Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro
 435 440 445
 Val Ser Pro Ser Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His
 450 455 460
 Gln Gln Val Ser His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro
 465 470 475 480
 Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys
 485 490 495
 Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp
 500 505 510
 Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu
 515 520 525
 Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn
 530 535 540
 Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met
 545 550 555 560
 Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys
 565 570 575
 Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val
 580 585 590
 Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu
 595 600 605
 Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys
 610 615 620
 Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys Ile Val Asn Leu
 625 630 635 640
 Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile
 645 650 655
 Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val
 660 665 670

Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg
675 680 685

Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu
690 695

<010> 178
<011> 662
<012> PRT
<013> Homo sapiens

<400> 178

Met Ala Arg Pro Ser Ser Glu Leu Leu Glu Lys Tyr His Ile Ile Asp
1 5 10 15

Gln Phe Leu Ser His Gly Ile Lys Thr Ile Ile Asn Leu Gln Arg Pro
20 25 30

Gly Glu His Ala Ser Cys Gly Asn Pro Leu Glu Gln Glu Ser Gly Phe
35 40 45

Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly Ile Tyr Phe Tyr Asn
50 55 60

Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu Thr Thr Ile Leu Asp
65 70 75 80

Met Val Lys Val Met Thr Phe Ala Leu Gln Glu Gly Lys Val Ala Ile
85 90 95

His Cys His Ala Gly Leu Gly Arg Thr Gly Val Leu Ile Ala Cys Tyr
100 105 110

Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln Ala Ile Ile Phe Val
115 120 125

Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg Gly Gln Leu Leu Cys
130 135 140

Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu Arg Asn Ile Phe Ser
145 150 155 160

Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu Pro Gln Tyr Leu Ile
165 170 175

Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala Arg Leu Leu Lys His
180 185 190

Val Pro Lys Ile Ile His Leu Val Cys Lys Leu Leu Leu Asp Leu Ala
195 200 205

Glu Asn Arg Pro Val Met Met Lys Asp Val Ser Glu Gly Pro Gly Leu
210 215 220

Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met Val Thr Met Gln Leu
225 230 235 240

Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val Ser Asn Pro Pro Asn
 245 250 255
 Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Phe Ser
 260 265 270
 Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg Arg Asn Val Glu Cys
 275 280 285
 Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu Ser Tyr Ser Asp Ser
 290 295 300
 Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln Gly Glu Thr Pro Gln
 305 310 315 320
 Thr Val Pro Ala Gln Ile Leu Val Gly His Lys Pro Arg Gln Gln Lys
 325 330 335
 Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro Glu Pro Asp Leu His
 340 345 350
 Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe Trp Ser Gln Ser Lys
 355 360 365
 Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly Ser Pro Ile Phe His
 370 375 380
 Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly Ala Phe Ser Ala
 385 390 395 400
 Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser Pro Ser Phe
 405 410 415
 Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val Ser His
 420 425 430
 Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Arg Gln
 435 440 445
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Pro Lys
 450 455 460
 Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Leu Ser
 465 470 475 480
 Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Glu Ala
 485 490 495
 Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Ser Val
 500 505 510
 Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met Trp Gln Lys Glu Leu
 515 520 525
 Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys Gly Glu Arg Asp Pro
 530 535 540

Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val Glu Gln Leu Lys Glu
 545 555 555 560
 Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu Val Asp Arg Arg Ala
 565 570 575
 Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys Gly Gln His Gln Thr
 580 585 590
 Ile Leu Cys Val Leu His Cys Ile Val Asn Leu Gln Thr Ile Pro Val
 595 600 605
 Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile Lys Ala Phe Thr Lys
 610 615 620
 Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val Tyr Asn Thr Ile Lys
 625 630 635 640
 Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg Lys Met Thr Lys Asp
 645 650 655
 Gly Pro Lys Pro Gly Leu
 660

<210> 179
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized Oligonucleotide.

<400> 179
 ggauaucacu acugcauugc cugga

25

<210> 180
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized Oligonucleotide.

<400> 180
 uatagcagau cugugcaggc caggu

25

<210> 181
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized Oligonucleotide.

<400> 181 25
 ugumacaca guagcggaag augcu

<210> 182
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized Oligonucleotide.

<400> 182 25
 agguaguaga gaaugguuag ccuuc

<210> 183
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthesized Oligonucleotide.

<400> 183 25
 ugaaagcagg cgagauucga uccga

<210> 184
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 184 20
 actaccgct cacacgcttc

<210> 185
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 185 20
 attgactaca gcagggcttc

<210> 186
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 186 26
 atcaagtgtg acccagactg cctccg

<210> 187
 <211> 28

<212> DNA
 <213> Homo sapiens

<400> 187 28
 ccatatgggat ccatggccca tgagattg

<210> 188
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 188 30
 ggtaccctcg agtcaggaga cctcaatgat

<210> 189
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 189 30
 ggtaccctcg agtcaagtct ggttcttaat

<210> 190
 <211> 664
 <212> PRT
 <213> Homo sapiens

<400> 190

Met	Ala	His	Glu	Ile	Gly	Thr	Gln	Ile	Val	Thr	Glu	Arg	Leu	Val	Ala	15
1			5						10							
Leu	Leu	Glu	Ser	Gly	Thr	Glu	Lys	Val	Leu	Leu	Ile	Asp	Ser	Arg	Pro	30
		20						25								
Phe	Val	Glu	Tyr	Asn	Thr	Ser	His	Ile	Leu	Glu	Ala	Ile	Asn	Ile	Asn	45
		35					40									
Cys	Ser	Lys	Leu	Met	Lys	Arg	Arg	Leu	Gln	Gln	Asp	Lys	Val	Leu	Ile	60
		50				55										
Thr	Glu	Leu	Ile	Gln	His	Ser	Ala	Lys	His	Lys	Val	Asp	Ile	Asp	Cys	80
		65			70				75							
Ser	Gln	Lys	Val	Val	Val	Tyr	Asp	Gln	Ser	Ser	Gln	Asp	Val	Ala	Ser	95
			85					90								
Leu	Ser	Ser	Asp	Cys	Phe	Leu	Thr	Val	Leu	Leu	Gly	Lys	Leu	Glu	Lys	110
			100					105					110			
Ser	Phe	Asn	Ser	Val	His	Leu	Leu	Ala	Gly	Gly	Phe	Ala	Glu	Phe	Ser	125
		115				120						125				
Arg	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Ser	Thr	Leu	Val	Pro	Thr	

130	135	140
Cys Ile Ser Gln Pro	Cys Leu Pro Val Ala Asn Ile Gly Pro Thr Arg	
145	150	155 160
Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn Lys		
	165	170 175
Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser Asn		
	180	185 190
Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg Val		
	195	200 205
Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp Lys		
	210	215 220
Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val Leu		
225	230	235 240
Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile Ala		
	245	250 255
Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg Phe		
	260	265 270
Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Ser Phe Asn Phe Leu Gly		
	275	280 285
Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Ala Gly Ala Ser		
	290	295 300
Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn Glu		
305	310	315 320
Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro Leu		
	325	330 335
Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln Arg		
	340	345 350
Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro Ser		
	355	360 365
Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His Leu		
	370	375 380
Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe Ser		
385	390	395 400
Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu		
	405	410 415
His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro Ser		
	420	425 430
Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln		

435	440	445
Glu Leu Ser Glu Gln Thr	Pro Glu Thr Ser	Pro Asp Lys Glu Glu Ala
450	455	460
Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg	Pro Ser Asp Ser Gln Ser	
465	470	475 480
Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln Arg		
485	490	495
Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr		
500	505	510
His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr		
515	520	525
Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala		
530	535	540
Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr		
545	550	555 560
Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser Ala		
565	570	575
Ser Tyr Ser Ala Tyr Ser Arg Ser Gln Leu Pro Thr Cys Gly Asp Gln		
580	585	590
Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser		
595	600	605
Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg		
610	615	620
Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg		
625	630	635 640
Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly		
645	650	655
Ser Met Glu Ile Ile Glu Val Ser		
660		

<210> 191
 <211> 302
 <212> PRT
 <213> Homo sapiens

<400> 191

Met Ala His Glu Ile Val Gly Thr Gln Ile Val Thr Glu Arg Leu Val	
1 5 10 15	
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg	
20 25 30	

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile
 35 40 45
 Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu
 50 55 60
 Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp
 65 70 75 80
 Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala
 85 90 95
 Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu
 100 105 110
 Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe
 115 120 125
 Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro
 130 135 140
 Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr
 145 150 155 160
 Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn
 165 170 175
 Lys Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser
 180 185 190
 Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg
 195 200 205
 Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp
 210 215 220
 Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val
 225 230 235 240
 Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile
 245 250 255
 Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg
 260 265 270
 Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Ser Phe Asn Phe Leu
 275 280 285
 Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr
 290 295 300
 <110> 192
 <111> 20
 <112> PRT
 <113> Artificial Sequence
 <120>

<223> Synthesized Peptide.

<400> 193

Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys Ser Lys Lys Leu Lys Leu
1 5 10 15

Leu His Leu Glu
20

<210> 193

<211> 19

<212> PFT

<213> Artificial Sequence

<220>

<223> Synthesized Peptide.

<400> 193

Cys Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln Ser Lys Arg
1 5 10 15

Leu His Ser

<210> 194

<211> 21

<212> DNA

<213> Homo sapiens

<400> 194

ctggctgttg cactgcatag t

21

<210> 195

<211> 19

<212> DNA

<213> Homo sapiens

<400> 195

tgggcaaggga aagcttccct

19

<210> 196

<211> 26

<212> DNA

<213> Homo sapiens

<400> 196

aacctgcaga caattcccgt ggatgt

26

<210> 197

<211> 21

<212> DNA

<213> Homo sapiens

<400> 197	21
gaaatgccat tgetgaaatc c	
<210> 198	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 198	23
gactgcttgc tectgetcat agg	
<210> 199	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 199	23
cgactacgac ccggetccat cga	
<210> 200	
<211> 23	
<212> DNA	
<213> Homo sapiens	
<400> 200	23
aggagcagat ggtagacgtg ttc	
<210> 201	
<211> 20	
<212> DNA	
<213> Homo sapiens	
<400> 201	20
ggctcagggt ctggatcatg	
<210> 202	
<211> 25	
<212> DNA	
<213> Homo sapiens	
<400> 202	25
tgcgtgtrtat gcactccgga tgcac	
<210> 203	
<211> 25	
<212> DNA	
<213> Homo sapiens	
<400> 203	25
cacacaccaa atgtgtaaca gttca	

<210> 204
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 204
 gctactgctt tcctttctta aacatgt

27

<210> 205
 <211> 35
 <212> DNA
 <213> Homo sapiens

<400> 205
 cacttccaga gtgtgggtcat gccca

25

<210> 206
 <211> 321
 <212> PFT
 <213> Homo sapiens

<400> 206

Met	Glu	Met	Glu	Lys	Glu	Phe	Glu	Gln	Ile	Asp	Lys	Ser	Gly	Ser	Trp	
1				5					10					15		
Ala	Ala	Ile	Tyr	Gln	Asp	Ile	Arg	His	Glu	Ala	Ser	Asp	Phe	Pro	Cys	
		20						25					30			
Arg	Val	Ala	Lys	Leu	Pro	Lys	Asn	Lys	Asn	Arg	Asn	Arg	Tyr	Arg	Asp	
		35					40					45				
Val	Ser	Pro	Phe	Asp	His	Ser	Arg	Ile	Lys	Leu	His	Gln	Glu	Asp	Asn	
	50					55					60					
Asp	Tyr	Ile	Asn	Ala	Ser	Leu	Ile	Lys	Met	Glu	Glu	Ala	Gln	Arg	Ser	
65					70					75					80	
Tyr	Ile	Leu	Thr	Gln	Gly	Pro	Leu	Pro	Asn	Thr	Cys	Gly	His	Phe	Trp	
			85						90					95		
Glu	Met	Val	Trp	Glu	Gln	Lys	Ser	Arg	Gly	Val	Val	Met	Leu	Asn	Arg	
		100						105					110			
Val	Met	Glu	Lys	Gly	Ser	Leu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Gln	Lys	
		115					120					125				
Glu	Glu	Lys	Glu	Met	Ile	Phe	Glu	Asp	Thr	Asn	Leu	Lys	Leu	Thr	Leu	
		130				135					140					
Ile	Ser	Glu	Asp	Ile	Lys	Ser	Tyr	Tyr	Thr	Val	Arg	Gln	Leu	Glu	Leu	
145					150					155				160		

Glu Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe His Tyr
 165 170 175

Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu
 180 185 190

Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His
 195 200 205

Gly Pro Val Val Val His Ser Ser Ala Gly Ile Gly Arg Ser Gly Thr
 210 215 220

Phe Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp
 225 230 235 240

Pro Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Lys Phe
 245 250 255

Arg Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu
 260 265 270

Ala Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln
 275 280 285

Asp Gln Trp Lys Glu Leu Ser His Glu Asp Leu Glu Pro Pro Pro Gly
 290 295 300

His Ile Pro Pro Pro Pro Arg Pro Pro Lys Arg Ile Leu Glu Pro His
 305 310 315 320

Asn

<210> 207
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 207

Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu Ser
 1 5 10 15

Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu Val
 20 25 30

Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile Pro
 35 40 45

Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu Gly
 50 55 60

Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp Ser
 65 70 75 80

Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe Asn
 85 90 95

Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala Leu
 100 105 110

Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr Ser
 115 120 125

Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys Met
 130 135 140

Asp Val Lys Ser Ala Leu Ser Ile Val Arg Gln Asn Arg Glu Ile Gly
 145 150 155 160

Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg Leu
 165 170 175

Ala Lys Glu Gly Lys Leu Lys Pro
 180

<210> 208
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 208

Ala Ser Phe Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly Cys Ala
 1 5 10 15

Lys Asp Ser Thr Asn Leu Asp Val Leu Glu Glu Phe Gly Ile Lys Tyr
 20 25 30

Ile Leu Asn Val Thr Pro Asn Leu Pro Asn Leu Phe Glu Asn Ala Gly
 35 40 45

Glu Phe Lys Tyr Lys Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn
 50 55 60

Leu Ser Gln Phe Phe Pro Glu Ala Ile Ser Phe Ile Asp Glu Ala Arg
 65 70 75 80

Gly Lys Asn Cys Gly Val Leu Val His Ser Leu Ala Gly Ile Ser Arg
 85 90 95

Ser Val Thr Val Thr Val Ala Tyr Leu Met Gln Lys Leu Asn Leu Ser
 100 105 110

Met Asn Asp Ala Tyr Asp Ile Val Lys Met Lys Lys Ser Asn Ile Ser
 115 120 125

Pro Asn Phe Asn Phe Met Gly Gln Leu Leu Asp Phe Glu Arg Thr Leu
 130 135 140